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PAAD DOMAIN-CONTAINING POLYPEPTIDES, ENCODING
NUCLEIC ACIDS, AND METHODS OF USE

5

BACKGROUND OF THE INVENTION

FIELD OF THE INVENTION

10 This invention relates generally to the fields
of molecular biology and molecular medicine and more
specifically to the identification of proteins involved
in programmed cell death, cytokine processing and
receptor signal transduction, and associations of these
15 proteins.

BACKGROUND INFORMATION

Programmed cell death is a physiologic process
20 that ensures homeostasis is maintained between cell
production and cell turnover in essentially all self-
renewing tissues. In many cases, characteristic
morphological changes, termed "apoptosis," occur in a
dying cell. Since similar changes occur in different
25 types of dying cells, cell death appears to proceed
through a common pathway in different cell types.

In addition to maintaining tissue homeostasis,
apoptosis also occurs in response to a variety of
30 external stimuli, including growth factor deprivation,
alterations in calcium levels, free-radicals, cytotoxic
lymphokines, infection by some viruses, radiation and
most chemotherapeutic agents. Thus, apoptosis is an
inducible event that likely is subject to similar
35 mechanisms of regulation as occur, for example, in a
metabolic pathway. In this regard, dysregulation of

apoptosis also can occur and is observed, for example, in some types of cancer cells, which survive for a longer time than corresponding normal cells, and in neurodegenerative diseases where neurons die prematurely.

5 In viral infections, induction of apoptosis can figure prominently in the pathophysiology of the disease process, because immune-based eradication of viral infections depend on elimination of virus-producing host cells by immune cell attack resulting in apoptosis.

10

Some of the proteins involved in programmed cell death have been identified and associations among some of these proteins have been described. However, additional apoptosis regulating proteins remain to be
15 found and the mechanisms by which these proteins mediate their activity remains to be elucidated. The identification of the proteins involved in cell death and an understanding of the associations between these proteins can provide a means for manipulating the process
20 of apoptosis in a cell and, therefore, selectively regulating the relative lifespan of a cell or its relative resistance to cell death stimuli.

The identification of new proteins or new
25 domains within known proteins, and the elucidation of the proteins with which they interact, therefore, can form the basis for strategies designed to alter apoptosis, cytokine production, cytokine receptor signaling, and other cellular processes. Thus, a need exists to
30 identify novel apoptosis-related domains within both novel and known proteins. The present invention satisfies this need and provides additional advantages as well.

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SUMMARY OF THE INVENTION

The invention provides isolated nucleic acid molecules encoding PAAD-domain containing polypeptides and functional fragments thereof, including fragments containing PAAD domains, NB-ARC domains and LRR domains. Also provided are vectors containing such nucleic acid molecules and host cells containing the vectors. Also provided are oligonucleotides therefrom and methods of identifying nucleic acid molecules encoding a PAAD-containing polypeptide in a sample using such oligonucleotides.

Also provided are isolated PAAD-domain containing polypeptides and functional fragments thereof, including fragments containing PAAD domains, NB-ARC domains and LRR domains, and peptides therefrom.

The invention further provides antibodies that can specifically bind to PAAD-domain containing polypeptides, and methods of detecting PAAD-domain containing polypeptides in a sample using such antibodies.

Also provided is a method of identifying a polypeptide that associates with a PAAD-domain containing polypeptide or fragment thereof, including fragments containing PAAD domains, NB-ARC domains and LRR domains. The method is practiced by contacting a PAAD domain-containing polypeptide or fragment with a candidate PAAD domain-containing polypeptide-associated polypeptide (PAP), and detecting association of the PAAD domain-containing polypeptide or fragment with the candidate PAP, wherein a candidate PAP that associates with the polypeptide is identified as a PAP.

The invention also provides a method of identifying an effective agent that alters the association of a PAAD domain-containing polypeptide or fragment with a PAP. The method is practiced by

5 contacting a PAAD domain-containing polypeptide, or a PAAD, NB-ARC or LRR domain therefrom, and the PAP under conditions that allow the PAAD domain-containing polypeptide or fragment and the PAP to associate, with a candidate agent, and detecting the altered association of

10 the PAAD domain-containing polypeptide or domain with the PAP, wherein an agent that alters the association is identified as an effective agent.

Further provided is a method for identifying an

15 agent that associates with a PAAD-domain containing polypeptide or fragment therefrom, including a fragment containing a PAAD domain, NB-ARC domain or LRR domains. The method is practiced by contacting the PAAD domain-containing polypeptide or fragment with a candidate agent

20 and detecting association of the PAAD domain-containing polypeptide with the agent.

Also provided is a method of identifying an agent that modulates PAAD domain-mediated inhibition of

25 NFkB activity. The method is practiced by contacting a cell that recombinantly expresses a PAAD domain-containing polypeptide with a candidate agent and detecting NFkB activity in the cell. Increased or decreased NFkB activity in the cell compared to a control

30 cell indicates that the candidate agent is an agent that modulates PAAD domain-mediated inhibition of NFkB activity.

Further provided is a method of identifying an

35 agent that modulates an activity of a NB-ARC domain of a PAAD domain-containing polypeptide. The method is

practiced by contacting an NB-ARC domain-containing polypeptide with a candidate agent and detecting an activity of the NB-ARC domain, wherein an increase or decrease of the activity identifies the agent as an agent that modulates the activity of the NB-ARC domain. The detected activity of the NB-ARC domain can be selected from homo-oligomerization, hetero-oligomerization, nucleotide hydrolysis, and nucleotide binding.

Further provided is a method of modulating NFkB transcriptional activity in a cell. The method is practiced by introducing a nucleic acid molecule encoding a PAAD domain-containing polypeptide into a cell and expressing the nucleic acid molecule in the cell, wherein the expression of the nucleic acid modulates NFkB transcriptional activity in the cell.

The invention also provides a method of decreasing expression of a PAAD domain-containing polypeptide in a cell, by introducing an antisense or dsRNA nucleic molecule into a cell, wherein the antisense or dsRNA nucleic molecule binds to a nucleic acid molecule encoding a PAAD domain-containing polypeptide.

BRIEF DESCRIPTION OF THE FIGURES

Figure 1 shows that multiple alignment using the CLUSTAL W program (Higgins et al. Nuc. Acid Res. 22:4673-4680 (1995)) of the aligned part of selected members of the PAAD family from humans. NCBI gi accession numbers are included. The "sec_str" line shows secondary structure prediction made for pyrin using the PHD program (Rost et al., Comput. Appl. Biosci. 10:53-60 (1994)).

Figure 2 shows the evolutionary tree showing the relationship between selected members of the PAAD family of proteins from humans and viruses. The tree was built using the CLUSTALW program. Proteins containing NB-ARC (NACHT) NTP-ase domains as well as PAAD domains (NAC and PAN1-6) are shown in grey.

Figure 3 shows a schematic (not to scale) representation of domain arrangement in proteins containing a PAAD domain.

Figure 4 shows a model of the PAAD domain built on the template of the Death Effector Domain from FADD protein (PDB code: 1alz), using the FFAS alignment and the Modeller program (Sali et al, J. Mol. Biol. 234:779-815 (1993)). Some motifs identified in the sequence analyses of the PAAD family stand out as surface features that may be responsible for biological activity of these domains. A notable feature is the conserved Lys-Phe-Lys motif, that according to this model, is found on the protein surface, in helix 2. Positively charged residues from this motif, together with other charged residues from another, less conserved motif in helix 5, form a positively charged surface of the predicted protein that may be important for inter-molecule interaction. These residues are shown in the ball-and-stick representation.

Figure 5 shows a luciferase reporter assay in which NFkB transcription activity was determined in cells transfected with NIK, IKK α or IKK β and either an empty vector or the indicated amounts of a vector expressing PAN2.

Figure 6 shows a protein interaction assay in which vectors expressing Myc-tagged PAN2, or Myc-tagged domains of PAN2 as indicated, and either Flag-tagged IkB α

or Flag-tagged empty vector, were co-transfected into 293T cells. The lysates were immunoprecipitated with an anti-Flag antibody and blotted with either an anti-Myc or an anti-Flag antibody.

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Figure 7 shows a luciferase reporter assay in which NF κ B transcriptional activity was determined in cells transfected with Bcl10 (A), contacted with TNF α (B), contacted with IL-1 β (C), or transfected with Bcl10, 10 Nod1 or Cardiak (D), and further transfected with either an empty vector (CNTR), or vectors expressing ASC, domains therefrom, or ASC2, as indicated.

Figure 8 shows an immunoblot in which the 15 expression of TRAF1 and TRAF2 was examined in cells transfected with the indicated expression vectors and either stimulated with TNF or unstimulated. The expression of Tubulin was determined as a control.

20 Figure 9 shows the amount of interleukin-1 β secreted from 293N or Cos-7 cells transfected with the indicated expression vectors.

Figure 10 shows caspase activity, indicated by 25 the cleavage of the fluorogenic substrate Ac-DEVD-AFC over time in cells transfected with the indicated expression vectors. c/a indicates that the caspase is an active site mutant.

30 DETAILED DESCRIPTION OF THE INVENTION

In accordance with the present invention, there are provided PAAD domain-containing polypeptides and functional fragments thereof, encoding nucleic acid 35 molecules, and related compositions and methods. The

"PAAD domain" is an 80-100 residue domain named after the protein families in which it was first identified: pyrin, AIM (Absent-in-melanoma), ASC (apoptosis-associated speck-like protein containing a caspase recruitment domain), and death domain (DD)-like. The terms "PAAD" and "PACS" (for identified in Pyrin, AIM, Caspase, and Speck-like protein) are synonymous. Secondary structural predictions identify the PAAD domain as mostly helical (see Figure 1). The PAAD domain has the predicted tertiary structure shown in Figure 4, identifying PAAD as a member of the Death Domain (DD), Death Effector Domain (DED), Caspase Recruitment Domain (CARD) family. PAAD domains have been identified at the N-terminus of several different proteins involved in apoptosis, cancer, inflammation and immune responses, as described herein (see Figure 1).

Protein-protein interactions influence the activity of various proteins involved in apoptosis. Several protein interaction domains have been implicated in interactions among some apoptosis-regulating proteins. In accordance with the present invention, the PAAD domain has been identified at the N-terminus of the recently identified caspase-homologous gene from zebrafish (Inohara et al., Cell Death Differ, 7:509-510 (2000)), suggesting the involvement of the PAAD domain in apoptosis. In this protein, the PAAD domain occupies a position corresponding to the prodomain, which in other caspase genes is occupied by a CARD (caspase recruitment domain) or a DED (death effector domain) domain. Thus, it is contemplated herein that the PAAD domain functions as a death domain in apoptosis. Accordingly, methods are provided herein for identifying PAAD domain binding agents that modulate apoptotic activity.

As disclosed herein, PAAD domain-containing polypeptides bind proteins through their PAAD domains, including other PAAD domain-containing polypeptides, IKAP, Nod1, Cardiak, NIK and IKK-i.

5

Accordingly, methods are provided herein for identifying PAAD domain-associating proteins, and for identifying compounds that disrupt the interaction between the PAAD domain and PAAD domain-associating
10 proteins.

As disclosed herein, expression of the PAAD domain of PAAD domain-containing polypeptides is able to specifically modulate the induction of NF κ B activity by
15 various stimuli. NF κ B is the collective name for inducible dimeric transcription factors composed of members of the Rel family of DNA-binding proteins that recognize a common sequence motif. NF κ B is sequestered in the cytoplasm of resting cells through its association
20 with an inhibitory protein called I κ B. When stimulated by a variety of extracellular modulators, including the proinflammatory cytokines TNF α and IL-1, T- and B-cell mitogens, bacteria, bacterial lipopolysaccharide (LPS), viruses, viral proteins, double stranded RNA, and
25 physical and chemical stresses, a cascade of adaptor proteins and protein kinases is activated, leading to phosphorylation of I κ B by the I κ B kinases α and β (IKK α/β). I κ B phosphorylation leads to its ubiquitination, which targets the protein for rapid
30 degradation by the 26S proteasome. The degradation of I κ B exposes the nuclear localization signal (NLS) of NF κ B, resulting in NF κ B translocation to the nucleus and activation.

35

Active NFkB regulates the transcription of a large number of genes, including those involved in immune and inflammatory responses such as immunoreceptors, cell adhesion molecules, cytokines and chemokines. NFkB also
5 plays an important role in the antiviral response through interferon gene induction. Through adaptation, many viruses that do not cause interferon induction exploit NFkB to activate their own genes and to stimulate the survival and proliferation of lymphoid cells in which
10 they replicate.

NFkB can have either positive and negative effects on cellular apoptosis depending on the cell type, apoptotic stimulus, and timing of NFkB activation. NFkB
15 regulates the transcription of a variety of genes involved in blocking apoptosis, including cellular inhibitor of apoptosis (cIAP)-1, cIAP-2, TRAF1, TRAF2, superoxide dismutase (SOD), A20, and the Bcl-2 homolog Bfl-1/A1.

20

Inappropriate regulation of NFkB is involved in a wide range of human disorders, including cancers, neurodegenerative disorders, ataxia-telangiectasia, arthritis, asthma, inflammatory bowel disease and
25 numerous other inflammatory conditions (see Karin et al., Ann. Rev. Immunol. 18:621-663 (2000), and references therein). Activation of NFkB also correlates with resistance to apoptosis induced by cancer therapeutic agents.

30

Accordingly, methods are provided herein to identify agents that modulate, either positively or negatively, the PAAD domain-mediated modulation of NFkB activation. Such agents can thus be used to regulate
35 inflammatory responses, immune responses (including

autoimmune responses), apoptosis, and other processes mediated at least in part by NF κ B activity.

Further, PAAD domain-containing polypeptides are contemplated herein as influencing a variety of cellular and biochemical processes beyond apoptosis, including cell adhesion, inflammation and cytokine receptor signaling, and responses to viruses and infectious agents.

10

Exemplary invention PAAD domain-containing polypeptides include a family of proteins that in addition to a PAAD domain, contain a domain similar to the recently identified NB-ARC (NACHT) NTP-ase family (Koonin et al., Trends Biochem Sci, 25:223-224 (2000)) (see Figure 3). The NACHT domain has been implicated in nucleotide binding, oligomerization, and nucleotide (e.g. ATP and/or GTP) hydrolysis. This family of proteins is referred to herein as PAAD and Nucleotide-binding ("PAN") proteins. The amino acid sequence of the PAAD domains of PAN1 through PAN6 are set forth in Figure 1 and as SEQ ID NOS:1-6, respectively.

The sequences of PAN2-6 cDNAs and encoded polypeptides are set forth as follows: PAN2: SEQ ID NOS:15 and 16; PAN3: SEQ ID NOS:17 and 18; PAN4: SEQ ID NOS:19 and 20; PAN5: SEQ ID NOS:21 and 22; PAN6: SEQ ID NOS:23 and 24.

Other invention PAAD domain-containing polypeptides include pyrin2 and human ASC2, whose PAAD domain sequences are set forth in Figure 1 and as SEQ ID NOS:8 and 10, respectively. The sequences of pyrin2 cDNA and encoded polypeptide are set forth as SEQ ID NOS:25 and 26. A 719 residue open reading frame from chromosome 1, which is identical over the N-terminal 41 amino acids

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with SEQ ID NO:26, has been identified and deposited as gi:14731966 (SEQ ID NOS:58 and 59). Accordingly, a PAAD domain-containing polypeptide can contain the first 41 amino acids of SEQ ID NO:26, and can optionally further
5 comprise the amino acid sequence designated SEQ ID NO:59.

The sequences of ASC2 cDNA and encoded polypeptide are set forth as SEQ ID NOS:27 and 28. ASC2 is an 89-residue protein containing only the PAAD domain.
10

In accordance with the present invention, the PAAD domain has also been identified in the N-terminal part of "Absent in Melanoma-2" (AIM2) and several closely homologous human and murine proteins, such as interferon-
15 inducible genes IFI16 and MNDA (DeYoung et al., Oncogene, 15:453-457 (1997) (see Figure 1; SEQ ID NOS:12 and 13). Proteins from this family were characterized as containing one or more copies of a conserved 200-residue domain, implicated in transcription repression (Johnstone
20 et al., J Biol Chem. 273:17172-17177 (1998). The N-terminal part of AIM2 and related homologous proteins, containing the invention PAAD domain was not functionally analyzed, with two exceptions. In MNDA protein, it was shown that the N-terminal domain is partly responsible
25 for homodimerization (Xie et al., FEBS Lett. 408:151-155 (1997). In IFI16, DNA-binding was attributed to a 159-residue long N-terminal segment (Dawson et al. Biochem Biophys Res Commun, 214:152-162 (1995)). There are also two viral proteins homologous to the interferon-inducible
30 MNDA/IFI16 family, (M013L from myxoma virus and gp013L from rabbit fibroma virus), that contain an invention PAAD domain. The PAAD domain of M013L is shown in Figure 1 (SEQ ID NO:14).

35 In accordance with the present invention, a PAAD domain has also been identified in the N-terminus of

the ASC protein (apoptosis-associated speck-like protein containing a CARD) (Masumoto et al., J Biol Chem, 274:33835-33838 (1999)) (see Figure 1; SEQ ID NO:9). . The ASC protein was identified by characteristic dot-like
5 aggregates (specks) which were present in cells during apoptosis triggered by retinoic acid and other anti-cancer drugs (Masumoto et al., supra (1999)). The C-terminal half of the speck protein contains an easily recognizable CARD domain, while the N-terminal half has
10 now been found to be occupied by an invention PAAD domain.

One of the PAAD domain-containing polypeptides, PAN6 (SEQ ID NO:24), allowed an independent and
15 unambiguous connection between the pyrin/ASC/caspase and the AIM2/IFI16 branches of the family. Three iterations of a standard PSI-BLAST search against the NCBI nr database starting from this putative domain pulled out, among others, pyrin and AIM2, with E-values of 1e-23 and
20 1e-18, respectively.

The average sequence similarity between different branches of the PAAD domain protein family is approximately 25% of sequence identity (see Figure 1).
25 However, clear amino acid regions of strong sequence similarity are conserved throughout the PAAD domain family of proteins.

Accordingly, in one embodiment, invention PAAD
30 domains comprise the following amino acid consensus sequence motif -KFKX₁X₂L- (SEQ ID NO:29), where X₁ and X₂ can be any amino acid. Preferably, X₁ is selected from amino acids F, M, L, Y, E, H, Q and S, and X₂ is preferably selected from amino acids K, H, L, Y and F.
35 This motif has been found to be present in the N-terminal

half of the majority of invention PAAD domains (see, e.g., Figure 1).

In another embodiment, invention PAAD domains
5 are also contemplated herein comprising the following amino acid consensus sequence motif -KLKX₁X₂L- (SEQ ID NO:30), where X₁ and X₂ can be any amino acid. Preferably, X₁ is selected from amino acids F, M, L, Y, E, H, Q and S, and X₂ is preferably selected from amino acids
10 K, H, L, Y and F.

In yet another embodiment, invention PAAD domains are also contemplated herein comprising the following amino acid consensus sequence motif -RFRX₁X₂L-
15 (SEQ ID NO:31), where X₁ and X₂ can be any amino acid. Preferably, X₁ is selected from amino acids F, M, L, Y, E, H, Q and S, and X₂ is preferably selected from amino acids K, H, L, Y and F.

20 In yet another embodiment, invention PAAD domains are also contemplated herein comprising the following amino acid consensus sequence motif -RFKX₁X₂L- (SEQ ID NO:32), where X₁ and X₂ can be any amino acid. Preferably, X₁ is selected from amino acids F, M, L, Y, E,
25 H, Q and S, and X₂ is preferably selected from amino acids K, H, L, Y and F.

In yet another embodiment, invention PAAD domains are also contemplated herein comprising the
30 following amino acid consensus sequence motif -KFRX₁X₂L- (SEQ ID NO:33), where X₁ and X₂ can be any amino acid. Preferably, X₁ is selected from amino acids F, M, L, Y, E, H, Q and S, and X₂ is preferably selected from amino acids K, H, L, Y and F.

In still another embodiment, invention PAAD domains are also contemplated herein comprising the following amino acid consensus sequence motif -KFKX₁X₂I- (SEQ ID NO:34), where X₁ and X₂ can be any amino acid.

5 Preferably, X₁ is selected from amino acids F, M, L, Y, E, H, Q and S, and X₂ is preferably selected from amino acids K, H, L, Y and F.

Accordingly, there are provided PAAD domain-
10 containing polypeptides comprising an amino acid consensus sequence selected from the group consisting of:

-KFKX₁X₂L- (SEQ ID NO:29);
-KLKX₁X₂L- (SEQ ID NO:30);
-RFRX₁X₂L- (SEQ ID NO:31);
15 -RFXK₁X₂L- (SEQ ID NO:32);
-KFRX₁X₂L- (SEQ ID NO:33); and
-KFKX₁X₂I- (SEQ ID NO:34);

where X₁ and X₂ can be any amino acid. Preferably, X₁ is
20 selected from amino acids F, M, L, Y, E, H, Q and S, and X₂ is preferably selected from amino acids K, H, L, Y and F.

PAAD domains can be present in an invention
25 polypeptide fragment or chimeric protein in conjunction with other types of functional domains, thus providing a mechanism for bringing one or more functional domains into close proximity or contact with a target protein via PAAD:PAAD associations involving two PAAD-containing
30 polypeptides. For example, the PAAD domains of invention PAN proteins (e.g., PAN-1 through PAN6) allows invention PAN proteins to self-associate forming homo- or hetero-oligomers, thereby forming an oligomeric complex which brings proteins associated with PAN proteins into close
35 proximity to each other. Because some PAAD domain-containing proteins also contain a CARD domain, exemplary

proteins that are contemplated for association with invention PAN proteins are pro-caspases. Because most pro-caspases possess at least a small amount of protease activity even in their unprocessed form, the assembly of
5 a complex that brings the proforms of caspase into juxtaposition can result in trans-processing of zymogens, producing the proteolytically processed and active caspase. Thus, invention PAN proteins can employ a PAAD domain for self-oligomerization and a CARD domain for
10 binding a pro-caspase, resulting in caspase clustering, proteolytic processing and activation. In addition to the ability to activate caspases, PAAD domains are contemplated herein as being able to inhibit caspases.

15 In addition to their role in regulation of cell death and cell proliferation, PAAD domains can regulate other cellular processes. A PAAD domain-containing polypeptide can, for example, induce activation of the transcription factor NF-kB. Though caspase activation
20 resulting from PAAD domain interactions can be involved in inducing apoptosis, other caspases can be primarily involved in proteolytic processing and activation of inflammatory cytokines (such as pro-IL-1b and pro-IL-18). Thus, PAAD domain-containing polypeptides can also be
25 involved in cytokine receptor signaling, cytokine production and cJun N-terminal kinase activation, and, therefore, can be involved in regulation of immune and inflammatory responses.

30 In view of the function of the PAAD domain within the invention PAAD domain-containing polypeptides or functional fragments thereof, polypeptides of the invention are contemplated herein for use in methods to alter cellular and biochemical processes such as
35 apoptosis, NF-kB induction, cytokine processing, cytokine receptor signaling, caspase-mediated proteolysis, or cJun

N-terminal kinase activation, thus having modulating effects on cell life and death (i.e., apoptosis), inflammation, cell adhesion, or other cellular or biochemical processes.

5

Invention PAAD domain-containing polypeptides or functional fragments thereof are also contemplated in methods to identify PAAD domain binding agents and PAAD-associated polypeptides (PAPs) that alter apoptosis, NF-
10 kB induction, cytokine processing, cytokine receptor signaling, caspase-mediated proteolysis, or cJun N-terminal kinase activation, thus having modulating effects on cell life and death (i.e., apoptosis), inflammation, cell adhesion, or other cellular or
15 biochemical processes.

It is also contemplated herein that invention PAAD domain-containing polypeptides can associate with other PAAD domain-containing polypeptides to form
20 invention hetero-oligomers or homo-oligomers, such as heterodimers or homodimers. In particular, the association of the PAAD domain of invention polypeptides with another PAAD domain-containing polypeptide, such as those identified herein, including homo-oligomerization,
25 is sufficiently specific such that the bound complex can form *in vivo* in a cell or *in vitro* under suitable conditions. Similarly therefore, an invention PAAD domain-containing polypeptide can associate with another PAAD domain-containing polypeptide by PAAD:PAAD
30 interaction to form invention hetero-oligomers or homo-oligomers, such as heterodimers or homodimers.

In addition to PAAD domains, an invention PAAD domain-containing polypeptide can contain a variety of
35 additional domains including a CARD domain, a NB-ARC domain, a LRR domain, a caspase protease domain, or other

recognized domains (see Figure 3). Accordingly, PAAD domain-containing polypeptides can exhibit one or more of the biological activities characteristic of known CARD domain-, NB-ARC domain-, LRR domain-, or caspase domain-
5 containing polypeptides.

A PAAD domain-containing polypeptide that contains a caspase recruitment domain, or CARD domain (e.g. ASC; Figure 3), can associate with pro-caspases,
10 caspases or with caspase-associated proteins, thereby altering caspase proteolytic activity.

A PAAD domain-containing polypeptide that contains a caspase protease domain (e.g. zebrafish
15 caspase; Figure 3) can hydrolyze amide bonds, particularly the amide bond of a peptide or polypeptide backbone. Typically, a caspase protease domain contains a P20/P10 domain in the active site region of the caspase protease domain. Thus, a caspase protease domain has
20 proteolytic activity.

Caspase proteolytic activity is associated with apoptosis of cells, and additionally with cytokine production. As used herein a "caspase" is any member of
25 the cysteine aspartyl proteases. A "pro-caspase" is an inactive or less-active precursor form of a caspase, which is typically converted to the more active caspase form by a proteolytic event, often preceded by a protein:protein interaction, such as an interaction with
30 a PAAD domain-containing polypeptide.

A PAAD domain-containing polypeptide that contains a NB-ARC domain (such as a PAN, or NAC; Figure 3) can associate with other polypeptides, particularly
35 with polypeptides comprising NB-ARC domains. Thus, an NB-ARC domain of an invention PAN associates with NB-ARC

domain-containing polypeptides by way of NB-ARC:NB-ARC association. Further, a NB-ARC domain demonstrates both nucleotide-binding (e.g., ATP-binding) and hydrolytic activities, which is typically required for its ability to associate with NB-ARC domain-containing polypeptides. Thus, an NB-ARC domain of an invention PAN protein comprises one or more nucleotide binding sites. As used herein, a nucleotide binding site is a portion of a polypeptide that specifically binds a nucleotide such as, e.g., ADP, ATP, and the like. Typically, the nucleotide binding site of NB-ARC will comprise a P-loop, a kinase 2 motif, or a kinase 3a motif of the invention PAAD domain-containing polypeptide (these motifs are defined, for example, in van der Biezen and Jones, Curr. Biol. 8:R226-R227 (1998)). Preferably, the nucleotide binding site of the NB-ARC of an invention PAN protein comprises a P-loop. The NB-ARC domain of the an invention PAN, therefore, is capable of associating with other NB-ARC domains in homo- or hetero-oligomerization. Additionally, the NB-ARC domain is characterized by nucleotide hydrolysis activity, which can influence the ability of an NB-ARC domain to associate with another NB-ARC domain. In accordance with the present invention, functional fragments of PAN proteins comprising NB-ARC domains are provided.

The amino acid sequences of NB-ARC domains of PAN2, 3, 5 and 6 are set forth as follows: PAN2, SEQ ID NO:37, corresponding to amino acids 147-465 of SEQ ID NO:16; PAN3, SEQ ID NO:60, corresponding to amino acids 196-512 of SEQ ID NO:18; PAN5, SEQ ID NO:62, corresponding to amino acids 93-273 of SEQ ID NO:22; and PAN6, SEQ ID NO:63, corresponding to amino acids 183-372 of SEQ ID NO:24. The skilled person can readily determine the NB-ARC domain amino acid sequences from other invention PAN polypeptides.

An invention PAAD domain-containing polypeptide, such as a PAN, therefore, is capable of PAAD:PAAD association and/or NB-ARC:NB-ARC association, resulting in a multifunctional polypeptide capable of one
5 or more specific associations with other polypeptides.

As used herein, the term "associate" or "association" refers to binding that is sufficiently specific such that a bound complex can form *in vivo* in a
10 cell or *in vitro* under suitable conditions.

A PAAD domain-containing polypeptide can also contain a Leucine-Rich Repeat (LRR) domain (e.g. PAN2, PAN3, PAN6, NAC; see Figure 3). Leucine-rich repeats
15 (LRRs) are 22-28 amino acid-long leucine rich sequence motifs found in cytoplasmic, membrane and extracellular proteins, including the mammalian Ced4 proteins Nod1 (Inohara et al., J. Biol. Chem. 274:14560-14567 (1999)) and DEFCAP, Hlaing et al., J. Biol. Chem. 276:9230-9238
20 (2001), NAC (Chu et al., J. Biol. Chem. 276:9239-9245 (2001), and Toll-like receptors (Takeuchi et al., Gene 231:59-65 (1999)). The biological activities of LRR domains can include, for example, protein-protein interactions that regulate signal transduction and cell
25 adhesion; assisting in formation of large, multiprotein complexes; and binding molecules produced by pathogens (e.g. lipids, RNA, proteins, DNA). For example, other LRR-containing proteins are known to bind bacterial lipopolysaccharide (e.g. TLR4 and Nod1/2), CpG DNA (e.g.
30 TLR9), the bacterial protein flagellin (e.g. TLR5), and steroids (e.g. plant LRRs) (see, for example, Fumitaka et al., Nature 410:1099-1103 (2001); Aderem et al., Nature 406:782-787 (2000); and Beutler, Immunity 15:5-14 (2001)). In accordance with the present invention,
35 functional fragments of PAN proteins comprising LRR domains are provided.

The amino acid sequences of the LRR domains of PAN2, 3 and 6 are set forth as follows: PAN2, SEQ ID NO:39, corresponding to amino acids 620-995 of SEQ ID NO:16; PAN3, SEQ ID NO:61, corresponding to amino acids 658 through the C-terminus of SEQ ID NO:18; and PAN6, SEQ ID NO:64, corresponding to amino acids 429-1031 of SEQ ID NO:24. The skilled person can readily determine the LRR domain amino acid sequences from other invention PAN polypeptides.

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A PAAD domain-containing polypeptide can also contain an "ANGIO-R" domain. An ANGIO-R domain is a region of a polypeptide chain that bears substantial similarity (e.g. 25, 30, 40% or higher sequence identity) to a portion of the 514-residue long protein "angiotensin II/vasopressin receptor" (described in Ruiz-Opazo et al., Nature Med. 1:1074-1081 (1995)).

The amino acid sequence of the ANGIO-R domain of PAN2 is set forth as SEQ ID NO:38, corresponding to amino acids 336-605 of SEQ ID NO:16.

An invention PAAD domain-containing polypeptide can alter cell processes such as apoptosis. For example, it is contemplated herein that an invention PAAD domain-containing polypeptide can increase apoptosis in a cell. It is also contemplated herein that an invention PAAD domain-containing polypeptide can decrease the level of apoptosis in a cell. For example, a PAAD domain-containing polypeptide which does not induce apoptosis may form hetero-oligomers with a PAAD domain-containing polypeptide which is apoptotic, thus interfering with its apoptosis-inducing activity.

35 In one embodiment, the invention provides PAAD domain-containing polypeptides comprising substantially

the same, or the same, amino acid sequence as set forth in any of SEQ ID NOS:16, 18, 20, 22, 24, 26 and 28, and fragments therefrom, including PAAD, NB-ARC and LRR domain-containing fragments.

5

As employed herein, the term "substantially the same amino acid sequence" refers to amino acid sequences having at least about 70% or 75% identity with respect to the reference amino acid sequence and retaining
10 comparable functional and biological activity characteristic of the polypeptide defined by the reference amino acid sequence. Preferably, polypeptides having "substantially the same amino acid sequence" will have at least about 80%, 82%, 84%, 86% or 88%, more
15 preferably 90%, 91%, 92%, 93% or 94% amino acid identity with respect to the reference amino acid sequence; with greater than about 95%, 96%, 97%, 98% or 99% amino acid sequence identity being especially preferred. It is recognized, however, that polypeptides containing less
20 than the described levels of sequence identity arising as splice variants or that are modified by conservative amino acid substitutions, or by substitution of degenerate codons are also encompassed within the scope of the present invention.

25

The term "biologically active" or "functional", when used herein as a modifier of invention PAAD domain-containing polypeptide, functional fragments thereof, or chimeric proteins, refers to a polypeptide that exhibits
30 functional characteristics similar to at least a portion of a naturally occurring PAAD domain-containing protein. Biological activities of a naturally occurring PAAD domain-containing protein include, for example, the ability to bind, preferably *in vivo*, to a nucleotide, to
35 a PAAD domain-containing polypeptide, to a CARD-containing polypeptide, to a NB-ARC-containing

polypeptide, to a LRR-containing polypeptide or to homo-oligomerize, or to alter protease activation, particularly caspase activation, or to catalyze reactions such as proteolysis or nucleotide hydrolysis, or to alter
5 NF- κ B activity, or to alter cJun N-terminal kinase activity, or to alter apoptosis, cytokine processing, cytokine receptor signaling, inflammation, immune response, or other biological activities described herein. Another biological activity of a PAAD domain-
10 containing polypeptide is the ability to act as an immunogen for the production of polyclonal and monoclonal antibodies that bind specifically to an invention PAAD domain-containing polypeptide.

15 A further biological activity of a PAAD domain-containing polypeptide is the ability to modulate the NF κ B transcriptional activity induced by a variety of stimuli, including activators of the TNF α and IL-1 β signaling pathways (see Examples). The PAAD domain is
20 sufficient for this activity.

The ability of a PAAD domain-containing polypeptide to bind another polypeptide such as a PAAD-associated polypeptide can be assayed using *in vitro* or
25 *in vivo* methods. For example, methods well known in the art such as yeast two-hybrid assays, co-immunoprecipitation, GST fusion co-purification, GST pull-down assays, and other methods provided in standard technique manuals such as Sambrook et al., Molecular
30 Cloning: A Laboratory Manual, 2nd ed., Cold Spring Harbor Press, Plainview, New York (1989) and , Ausubel et al., Current Protocols in Molecular Biology, John Wiley & Sons, New York (2000) can be used.

35 As used herein, the term "substantially purified" means a polypeptide that is in a form that is

relatively free from contaminating lipids, polypeptides, nucleic acids or other cellular material normally associated with the polypeptide. A substantially purified PAAD domain-containing polypeptide can be
5 obtained by a variety of methods well-known in the art, e.g., recombinant expression systems described herein, precipitation, gel filtration, ion-exchange, reverse-phase and affinity chromatography, and the like. Other well-known methods are described in Deutscher et
10 al., "Guide to Protein Purification" Methods in Enzymology Vol. 182, (Academic Press, (1990)). The methods and conditions for biochemical purification of a polypeptide of the invention can be chosen by those skilled in the art, and purification monitored, for
15 example, by an immunological assay, binding assay, or a functional assay.

In addition to the ability of invention PAAD domain-containing polypeptides, or functional fragments
20 thereof, to interact with other, heterologous proteins (e.g. other PAAD domain-, LRR domain- or NB-ARC domain-containing polypeptides), invention PAAD-containing polypeptides have the ability to self-associate to form invention homo-oligomers such as homodimers. This
25 self-association is possible through interactions between PAAD domains, and also through interactions between CARD domains or NB-ARC domains. Further, self-association can take place as a result of interactions between LRR domains.

30

In accordance with the invention, there are also provided mutations of PAAD domain-containing polypeptides which have activity different than a predominant naturally occurring PAAD domain-containing
35 polypeptide activity. As used herein, a "mutation" can be any deletion, insertion, or change of one or more

amino acids within the predominant naturally occurring protein sequence (e.g., wild-type), and a "fragment" is any truncated form, either carboxy-terminal, amino-terminal, or both, of the predominant naturally occurring protein. Preferably, the different activity of the mutation or fragment is a result of the mutant polypeptide or fragment maintaining some but not all of the activities of the respective predominant naturally occurring PAAD domain-containing polypeptide.

For example, a functional fragment of an invention protein can contain one or more of the following: a PAAD domain, an NB-ARC domain, a LRR domain or an ANGIO-R domain. In a specific example, a functional fragment of a PAAD domain-containing polypeptide such as a PAN can contain a PAAD domain and LRR domain, but lack a functional NB-ARC domain. Such a fragment will maintain a portion of the predominant naturally occurring PAN activity (e.g., PAAD domain functionality), but not all such activities (e.g., lacking an active NB-ARC domain). The resultant fragment will therefore have an activity different than the predominant naturally occurring PAN activity. In another example, a functional fragment of a PAN protein might have only the NB-ARC domain, allowing it to interact with other NB-ARC domain proteins in forming homo-oligomers or hetero-oligomers. Thus, a functional fragment of a PAAD domain-containing protein or polypeptide is not required to contain a functional PAAD domain, but only to contain a functional domain from a naturally occurring PAAD domain-containing protein. In one embodiment, the activity of the fragment will be "dominant-negative." A dominant-negative activity will allow the fragment to reduce or inactivate the activity of one or more isoforms of a predominant naturally occurring PAAD domain-containing polypeptide.

Methods to identify additional invention PAAD domain-containing polypeptides and functional fragments thereof are well known in the art and are disclosed herein. For example, genomic or cDNA libraries, including universal cDNA libraries can be probed according to methods disclosed herein or other methods known in the art. Full-length polypeptide-encoding nucleic acids such as full-length cDNAs can be obtained by a variety of methods well-known in the art. For example, 5' and 3' RACE, methodology is well known in the art and described in Ausubel et al., supra, and the like.

In another embodiment of the invention, chimeric proteins are provided comprising a PAAD domain-containing polypeptide, or a functional fragment thereof, fused with another protein or functional fragment thereof. Functional fragments of a PAAD domain-containing polypeptide include, for example, NB-ARC, LRR, and ANGIO-R domains or other fragments that retain a biological activity of an invention containing polypeptide. Polypeptides with which the PAAD domain-containing polypeptide or functional fragment thereof are fused can include, for example, glutathione-S-transferase, an antibody, or other proteins or functional fragments thereof which facilitate recovery of the chimera. Further polypeptides with which a PAAD domain-containing polypeptide or functional fragment thereof are fused can include, for example, luciferase, green fluorescent protein, an antibody, or other proteins or functional fragments thereof which facilitate identification of the chimera. Still further polypeptides with which a PAAD-containing polypeptide or functional fragment thereof are fused will include, for example, the LexA DNA binding domain, ricin, α -sarcin, an antibody or fragment thereof, or other polypeptides which have therapeutic properties or other biological activity.

Further invention chimeric proteins contemplated herein are chimeric proteins wherein a functional fragment of a PAAD domain-containing polypeptide is fused with a catalytic domain or a protein interaction domain from a heterologous polypeptide. For example, chimeric proteins can contain a functional fragment of a PAAD domain-containing polypeptide of the invention fused with a domain of a protein known in the art, such as CED-4, Apaf-1, caspase-1, and the like. For example, the NB-ARC domain of an invention PAN can be replaced by the NB-ARC domain of CED-4 and the like. Another example of such a chimera is a polypeptide wherein the CARD domain of an invention PAN is replaced by the CARD domain from CED-4, and the like. In a further example, an NB-ARC domain can be fused with a P20/P10 domain to form a novel chimera with caspase activity. In another embodiment, a chimeric protein can be formed which contains functional domains of 2 or more PAAD domain-containing polypeptides of the invention.

As used herein, the term "polypeptide" when used in reference to a PAAD domain-containing polypeptide is intended to refer to a peptide or polypeptide of two or more amino acids. The term "polypeptide analog" includes any polypeptide having an amino acid residue sequence substantially the same as a sequence specifically described herein in which one or more residues have been conservatively substituted with a functionally similar residue and which displays the ability to functionally mimic a PAAD domain-containing polypeptide as described herein. A "modification" of an invention polypeptide also encompasses conservative substitutions of an invention polypeptide amino acid sequence. Conservative substitutions of encoded amino acids include, for example, amino acids that belong within the following groups: (1) non-polar amino acids

(Gly, Ala, Val, Leu, and Ile); (2) polar neutral amino acids (Cys, Met, Ser, Thr, Asn, and Gln); (3) polar acidic amino acids (Asp and Glu); (4) polar basic amino acids (Lys, Arg and His); and (5) aromatic amino acids (Phe, Trp, Tyr, and His). Other groupings of amino acids can be found, for example in Taylor, J. Theor. Biol. 119:205-218 (1986), which is incorporated herein by reference. Other minor modifications are included within invention polypeptides so long as the polypeptide retains some or all of its function as described herein.

The amino acid length of functional fragments or polypeptide analogs of the present invention can range from about 5 amino acids up to the full-length protein sequence of an invention PAAD domain-containing polypeptide. In certain embodiments, the amino acid lengths include, for example, at least about 10 amino acids, at least about 15, at least about 20, at least about 25, at least about 30, at least about 35, at least about 40, at least about 45, at least about 50, at least about 55, at least about 60, at least about 65, at least about 70, at least about 75, at least about 80, at least about 85, at least about 90, at least about 95, at least about 100, at least about 125, at least about 150, at least about 175, at least about 200, at least about 250 or more amino acids in length up to no more than 1 residue less than a full-length naturally occurring PAAD domain-containing protein. In a particular embodiment of the invention, PAAD domain-containing functional fragments comprise an amino acid consensus sequence selected from the group consisting of:

- KFKX₁X₂L- (SEQ ID NO:29);
- KLKX₁X₂L- (SEQ ID NO:30);
- RFRX₁X₂L- (SEQ ID NO:31);
- RFKX₁X₂L- (SEQ ID NO:32);
- KFRX₁X₂L- (SEQ ID NO:33); and

-KFKX₁X₂I- (SEQ ID NO:34);

where X₁ and X₂ can be any amino acid. Preferably, PAAD domain-containing functional fragments comprise 15 or
5 more contiguous amino acids selected from the group consisting of SEQ ID NOS:1-14.

A modification of a polypeptide can also include derivatives, analogues and functional mimetics
10 thereof, provided that such polypeptide displays a PAAD domain-containing polypeptide biological activity. For example, derivatives can include chemical modifications of the polypeptide such as alkylation, acylation, carbamylation, iodination, or any modification that
15 derivatizes the polypeptide. Such derivatized molecules include, for example, those molecules in which free amino groups have been derivatized to form amine hydrochlorides, p-toluene sulfonyl groups, carbobenzoxy groups, t-butyloxycarbonyl groups, chloroacetyl groups or
20 formyl groups. Free carboxyl groups can be derivatized to form salts, methyl and ethyl esters or other types of esters or hydrazides. Free hydroxyl groups can be derivatized to form O-acyl or O-alkyl derivatives. The imidazole nitrogen of histidine can be derivatized to
25 form N-im-benzylhistidine. Also included as derivatives or analogues are those peptides which contain one or more naturally occurring amino acid derivatives of the twenty standard amino acids, for example, 4-hydroxyproline, 5-hydroxylysine, 3-methylhistidine, homoserine, ornithine
30 or carboxyglutamate, and can include amino acids that are not linked by peptide bonds. Polypeptides of the present invention also include any polypeptide having one or more additions and/or deletions of residues, relative to the sequence of a polypeptide whose sequence is shown herein,
35 so long as PAAD domain-containing polypeptide activity is maintained.

A modification of an invention polypeptide includes functional mimetics thereof. Mimetics encompass chemicals containing chemical moieties that mimic the function of the polypeptide. For example, if a
5 polypeptide contains two charged chemical moieties having functional activity, a mimetic places two charged chemical moieties in a spatial orientation and constrained structure so that the charged chemical function is maintained in three-dimensional space. Thus,
10 a mimetic, which orients functional groups that provide a function of a PAAD domain-containing polypeptide, are included within the meaning of a PAAD domain-containing polypeptide derivative. All of these modifications are included within the term "polypeptide" so long as the
15 invention polypeptide or functional fragment retains its function. Exemplary mimetics are peptidomimetics, peptoids, or other peptide-like polymers such as poly(α -amino acids), and also non-polymeric compounds upon which functional groups that mimic a peptide are positioned.

20
Another embodiment of the invention provides a PAAD domain-containing polypeptide, or a functional fragment thereof, fused with a moiety to form a conjugate. As used herein, a "moiety" can be a physical,
25 chemical or biological entity which contributes functionality to a PAAD domain-containing polypeptide or a functional fragment thereof. Functionalities contributed by a moiety include therapeutic or other biological activity, or the ability to facilitate
30 identification or recovery of a PAAD domain-containing polypeptide. Therefore, a moiety will include molecules known in the art to be useful for detection of the conjugate by, for example, by fluorescence, magnetic imaging, detection of radioactive emission. A moiety may
35 also be useful for recovery of the conjugate, for example a His tag or other known tags used for protein isolation

and/or purification, or a physical substance such as a bead. A moiety can be a therapeutic compound, for example, a cytotoxic drug which can be useful to effect a biological change in cells to which the conjugate
5 localizes.

An example of the methods for preparing the invention polypeptide(s) is to express nucleic acids encoding a PAAD domain-containing polypeptide in a
10 suitable host cell, such as a bacterial cell, a yeast cell, an amphibian cell such as an oocyte, or a mammalian cell, using methods well known in the art, and recovering the expressed polypeptide, again using well-known purification methods. Invention polypeptides can be
15 isolated directly from cells that have been transformed with expression vectors as known in the art. Recombinantly expressed polypeptides of the invention can also be expressed as fusion proteins with appropriate affinity tags, such as glutathione S transferase (GST) or
20 poly His, and affinity purified. The invention polypeptide, biologically functional fragments, and functional equivalents thereof can also be produced by *in vitro* transcription/translation methods known in the art, such as using reticulocyte lysates, as used for example,
25 in the TNT system (Promega). The invention polypeptide, biologically functional fragments, and functional equivalents thereof can also be produced by chemical synthesis. For example, synthetic polypeptides can be produced using Applied Biosystems, Inc. Model 430A or
30 431A automatic peptide synthesizer (Foster City, CA) employing the chemistry provided by the manufacturer.

The present invention also provides compositions containing an acceptable carrier and any of
35 an isolated, purified PAAD domain-containing mature protein, such as an invention PAN protein, or functional

polypeptide fragments thereof, alone or in combination with each other. These polypeptides or proteins can be recombinantly derived, chemically synthesized or purified from native sources. As used herein, the term

5 "acceptable carrier" encompasses any of the standard pharmaceutical carriers, such as phosphate buffered saline solution, water and emulsions such as an oil/water or water/oil emulsion, and various types of wetting agents.

10

The invention thus provides a therapeutic composition comprising a pharmaceutically acceptable carrier and a compound selected from the group consisting of a PAAD domain-containing fragment polypeptide, a PAAD
15 domain-containing chimeric protein, a PAAD domain-containing polypeptide modulating compound, and an anti-PAAD antibody. The invention additionally provides a method of treating a pathologies characterized by abnormal cell proliferation, abnormal cell death, or
20 inflammation by administering an effective amount of the composition containing a pharmaceutically acceptable carrier and a compound selected from the group consisting of a PAAD domain-containing polypeptide, a functional fragment thereof, a PAAD domain-containing polypeptide
25 modulating compound, and an anti-PAAD antibody.

PAAD domain-containing polypeptides can be administered to an individual to increase an activity associated with a PAAD domain-containing polypeptide,
30 including induction of apoptosis, functioning as a tumor suppressor, modulation of inflammation or cell adhesion, and the like. For example, a PAAD domain-containing polypeptide can be administered therapeutically to an individual using expression vectors containing nucleic
35 acids encoding PAAD domain-containing polypeptides, as described below. In addition, PAAD domain-containing

polypeptides, or a functional portion thereof, can be directly administered to an individual. Methods of administering therapeutic polypeptides are well known to those skilled in the art, for example, in the form of a pharmaceutical composition.

In accordance with another embodiment of the invention, there are provided isolated nucleic acids encoding a PAAD domain-containing polypeptide fragment or chimeric protein comprising a PAAD domain-containing polypeptide. The isolated nucleic acids can be selected from:

(a) DNA encoding a polypeptide containing the amino acid sequence set forth in SEQ ID NOS: 16, 18, 20, 22, 24, 26 or 28, or

(b) DNA that hybridizes to the DNA of (a) under moderately stringent conditions, where the DNA encodes a biologically active PAAD domain-containing polypeptide.

The nucleic acid molecules described herein are useful for producing invention polypeptides, when such nucleic acids are incorporated into a variety of protein expression systems known to those of skill in the art.

In addition, such nucleic acid molecules or fragments thereof can be labeled with a readily detectable substituent and used as hybridization probes for assaying for the presence and/or amount of an invention PAAD domain encoding gene or mRNA transcript in a given sample. The nucleic acid molecules described herein, and fragments thereof, are also useful as primers and/or templates in a PCR reaction for amplifying genes encoding invention polypeptides described herein.

The term "nucleic acid" or "nucleic acid molecule" (also referred to as polynucleotides)

encompasses ribonucleic acid (RNA) or deoxyribonucleic acid (DNA), probes, oligonucleotides, and primers and can be single stranded or double stranded. DNA can be either complementary DNA (cDNA) or genomic DNA, e.g. a PAAD domain encoding gene, and can represent the sense strand, the anti-sense strand, or both. Examples of nucleic acids are RNA, cDNA, or isolated genomic DNA encoding a PAAD domain-containing polypeptide. One means of isolating a PAAD domain encoding nucleic acid polypeptide is to probe a mammalian genomic or cDNA library with a natural or artificially designed DNA probe using methods well known in the art. DNA probes derived from the PAAD domain encoding gene are particularly useful for this purpose. DNA and cDNA molecules that encode PAAD domain-containing polypeptides can be used to obtain complementary genomic DNA, cDNA or RNA from mammalian (e.g., human, mouse, rat, rabbit, pig, and the like), or other animal sources, or to isolate related cDNA or genomic clones by screening cDNA or genomic libraries, using methods described in more detail below.

In one embodiment, invention nucleic acids comprise substantially the same or the same nucleotide sequence as set forth in SEQ ID NOs:15 (PAN2), 17 (PAN3), 19 (PAN4), 21 (PAN5), 23 (PAN6), 25 (pyrin2), or 27 (ASC2).

Thus a PAAD domain encoding nucleic acid as used herein refers to a nucleic acid encoding a polypeptide containing a PAAD domain-containing polypeptide fragment of the invention, or a PAAD domain-containing chimeric protein.

Use of the terms "isolated" and/or "purified" and/or "substantially purified" in the present specification and claims as a modifier of DNA, RNA,

polypeptides or proteins means that the DNA, RNA,
polypeptides or proteins so designated have been produced
in such form by the hand of man, and thus are separated
from their native in vivo cellular environment, and are
5 substantially free of any other species of nucleic acid
or protein. As a result of this human intervention, the
recombinant DNAs, RNAs, polypeptides and proteins of the
invention are useful in ways described herein that the
DNAs, RNAs, polypeptides or proteins as they naturally
10 occur are not.

Invention nucleic acids encoding PAAD domain-
containing polypeptides and invention PAAD domain-
containing polypeptides can be obtained from any species
15 of organism, such as prokaryotes, eukaryotes, plants,
fungi, vertebrates, invertebrates, and the like. A
particular species can be mammalian, e.g., human, rat,
mouse, rabbit, monkey, baboon, bovine, porcine, ovine,
canine, feline, and the like. A preferred PAAD domain
20 encoding nucleic acid herein, is human PAAD domain
encoding nucleic acid.

As employed herein, the term "substantially the
same nucleotide sequence" refers to DNA having sufficient
25 identity to the reference polynucleotide, such that it
will hybridize to the reference nucleotide under
moderately or highly stringent hybridization conditions.
In one embodiment, DNA having substantially the same
nucleotide sequence as the reference nucleotide sequence
30 encodes substantially the same amino acid sequence as
that set forth in any of SEQ ID NOs:16, 18, 20, 22, 24,
26 or 28. In another embodiment, DNA having
"substantially the same nucleotide sequence" as the
reference nucleotide sequence has at least 60%, or at
35 least 65% identity with respect to the reference
nucleotide sequence. DNA having at least 70%, 72%, 74%,

76%, 78%, 80%, 82%, 84%, 86% or 88%, more preferably at least 90%, 91%, 92%, 93% or 94% yet more preferably at least 95%, 96%, 97%, 98% or 99% identity to the reference nucleotide sequence is preferred.

5

As used herein, a "modification" of a nucleic acid can also include one or several nucleotide additions, deletions, or substitutions with respect to a reference sequence. A modification of a nucleic acid can include substitutions that do not change the encoded amino acid sequence due to the degeneracy of the genetic code. Such modifications can correspond to variations that are made deliberately, or which occur as mutations during nucleic acid replication.

15

Exemplary modifications of the recited nucleotide sequences include sequences that correspond to homologs of other species, including mammalian species such as mouse, primates, including monkey and baboon, rat, rabbit, bovine, porcine, ovine, canine, feline, or other animal species. The corresponding nucleotide sequences of non-human species can be determined by methods known in the art, such as by PCR or by screening genomic, cDNA or expression libraries.

25

Another exemplary modification of the invention PAAD domain encoding nucleic acid or PAAD domain-containing polypeptide can correspond to mutant or splice variant forms of the PAAD domain encoding nucleotide sequence. Additionally, a modification of a nucleotide sequence can include one or more non-native nucleotides, having, for example, modifications to the base, the sugar, or the phosphate portion, or having a modified phosphodiester linkage. Such modifications can be advantageous in increasing the stability of the nucleic acid molecule.

35

Furthermore, a modification of a nucleotide sequence can include, for example, a detectable moiety, such as a radiolabel, a fluorochrome, a ferromagnetic substance, a luminescent tag or a detectable binding agent such as biotin. Such modifications can be advantageous in applications where detection of a PAAD domain encoding nucleic acid molecule is desired.

This invention also encompasses nucleic acids which differ from the nucleic acids shown in SEQ ID NOs:15, 17, 19, 21, 23, 25 and 27, but which have the same phenotype. Phenotypically similar nucleic acids are also referred to as "functionally equivalent nucleic acids". As used herein, the phrase "functionally equivalent nucleic acids" encompasses nucleic acids characterized by slight and non-consequential sequence variations that will function in substantially the same manner to produce the same polypeptide product(s) as the nucleic acids disclosed herein. In particular, functionally equivalent nucleic acids encode polypeptides that are the same as those encoded by the nucleic acids disclosed herein or that have conservative amino acid variations. For example, conservative variations include substitution of a non-polar residue with another non-polar residue, or substitution of a charged residue with a similarly charged residue. These variations include those recognized by skilled artisans as those that do not substantially alter the tertiary structure of the protein.

30

Further provided are nucleic acids encoding invention PAAD domain-containing polypeptides that, by virtue of the degeneracy of the genetic code, do not necessarily hybridize to the invention nucleic acids under specified hybridization conditions. Preferred nucleic acids encoding the invention PAAD domain-

containing polypeptides are comprised of nucleotides that encode substantially the same amino acid sequence as set forth in SEQ ID NOs:16, 18, 20, 22, 24, 26 or 28.

5 Hybridization refers to the binding of complementary strands of nucleic acid (i.e., sense:antisense strands or probe:target-DNA) to each other through hydrogen bonds, similar to the bonds that naturally occur in chromosomal DNA. Stringency levels
10 used to hybridize a given probe with target-DNA can be readily varied by those of skill in the art.

 The phrase "stringent hybridization" is used herein to refer to conditions under which polynucleic
15 acid hybrids are stable. As known to those of skill in the art, the stability of hybrids is reflected in the melting temperature (T_m) of the hybrids. In general, the stability of a hybrid is a function of sodium ion concentration and temperature. Typically, the
20 hybridization reaction is performed under conditions of lower stringency, followed by washes of varying, but higher, stringency. Reference to hybridization stringency relates to such washing conditions.

25 As used herein, the phrase "moderately stringent hybridization" refers to conditions that permit target-nucleic acid to bind a complementary nucleic acid. The hybridized nucleic acids will generally have at least about 60% identity, at least about 75% identity, more at
30 least about 85% identity; or at least about 90% identity. Moderately stringent conditions are conditions equivalent to hybridization in 50% formamide, 5X Denhart's solution, 5X SSPE, 0.2% SDS at 42°C, followed by washing in 0.2X SSPE, 0.2% SDS, at 42°C.

The phrase "high stringency hybridization" refers to conditions that permit hybridization of only those nucleic acid sequences that form stable hybrids in 0.018M NaCl at 65°C, for example, if a hybrid is not
5 stable in 0.018M NaCl at 65°C, it will not be stable under high stringency conditions, as contemplated herein. High stringency conditions can be provided, for example, by hybridization in 50% formamide, 5X Denhart's solution, 5X SSPE, 0.2% SDS at 42°C, followed by washing in 0.1X
10 SSPE, and 0.1% SDS at 65°C.

The phrase "low stringency hybridization" refers to conditions equivalent to hybridization in 10% formamide, 5X Denhart's solution, 6X SSPE, 0.2% SDS at
15 22°C, followed by washing in 1X SSPE, 0.2% SDS, at 37°C. Denhart's solution contains 1% Ficoll, 1% polyvinylpyrrolidone, and 1% bovine serum albumin (BSA). 20X SSPE (sodium chloride, sodium phosphate, ethylene diamide tetraacetic acid (EDTA)) contains 3M sodium
20 chloride, 0.2M sodium phosphate, and 0.025 M (EDTA). Other suitable moderate stringency and high stringency hybridization buffers and conditions are well known to those of skill in the art and are described, for example, in Sambrook et al., supra (1989); and Ausubel et al.,
25 supra (2000).

Nucleic acids encoding polypeptides hybridize under moderately stringent or high stringency conditions to substantially the entire sequence, or substantial
30 portions, for example, typically at least 15, 17, 21, 25, 30, 40, 50 or more nucleotides of the nucleic acid sequence set forth in SEQ ID NOs:15, 17, 19, 21, 23, 25 or 27.

35 As used herein, the term "degenerate" refers to codons that differ in at least one nucleotide from a

reference nucleic acid, e.g., SEQ ID NOs:15, 17, 19, 21, 23, 25 and 27 but encode the same amino acids as the reference nucleic acid. For example, codons specified by the triplets "UCU", "UCC", "UCA", and "UCG" are
5 degenerate with respect to each other since all four of these codons encode the amino acid serine.

The invention also provides a modification of a nucleotide sequence that hybridizes to a PAAD domain
10 encoding nucleic acid molecule, for example, a nucleic acid molecule referenced as SEQ ID NOs:15, 17, 19, 21, 23, 25 or 27, under moderately stringent conditions. Modifications of nucleotide sequences, where the modification has at least 60% identity to a PAAD domain
15 encoding nucleotide sequence, are also provided. The invention also provides modification of a PAAD domain encoding nucleotide sequence having at least 65% identity, at least 70% identity, at least 72% identity, at least 74% identity, at least 76% identity, at least
20 78% identity, at least 80% identity, at least 82% identity, at least 84% identity, at least 86% identity, at least 88% identity, at least 90% identity, at least 91% identity, at least 92% identity, at least 93% identity, at least 94% identity, at least 95% identity,
25 at least 96% identity, at least 97% identity, at least 98% identity or at least 99% identity.

Identity of any two nucleic acid or amino acid sequences can be determined by those skilled in the art
30 based, for example, on known computer alignments such as BLAST 2.0, ClustalW and the like, which can be adjusted manually, if appropriate, to insert gaps to optimize the alignment according to standard practice in the art.

35 One means of isolating a nucleic acid encoding a PAAD domain-containing polypeptide is to probe a cDNA

library or genomic library with a natural or artificially designed nucleic acid probe using methods well known in the art. Nucleic acid probes derived from a PAAD domain encoding gene are particularly useful for this purpose.

5 DNA and cDNA molecules that encode PAAD domain-containing polypeptides can be used to obtain complementary genomic DNA, cDNA or RNA from mammals, for example, human, mouse, rat, rabbit, pig, and the like, or other animal sources, or to isolate related cDNA or genomic clones by the
10 screening of cDNA or genomic libraries, by methods well known in the art (see, for example, Sambrook et al., supra (1989); Ausubel et al., supra (2000)).

The invention additionally provides a nucleic
15 acid that hybridizes under high stringency conditions to the PAAD domain coding portion of any of SEQ ID NOs:15, 17, 19, 21, 23, 25 or 27. The invention also provides a nucleic acid having a nucleotide sequence substantially the same as set forth in any of SEQ ID NOs:15, 17,
20 19, 21, 23, 25 or 27.

The invention also provides a method for identifying nucleic acids encoding a mammalian PAAD domain-containing polypeptide by contacting a sample
25 containing nucleic acids with one or more invention oligonucleotides, wherein the contacting is effected under high stringency hybridization conditions, and identifying a nucleic acid that hybridizes to the oligonucleotide. The invention additionally provides a
30 method of detecting a PAAD domain encoding nucleic acid molecule in a sample by contacting the sample with two or more invention oligonucleotides, amplifying a nucleic acid molecule, and detecting the amplification. The amplification can be performed, for example, using PCR.
35 The invention further provides oligonucleotides that function as single stranded nucleic acid primers for

amplification of a PAAD domain encoding nucleic acid, wherein the primers comprise a nucleic acid sequence derived from the nucleic acid sequences set forth as SEQ ID NOS:SEQ ID NOS:15, 17, 19, 21, 23, 25 or 27.

5

In accordance with a further embodiment of the present invention, optionally labeled PAAD-encoding cDNAs, or fragments thereof, can be employed to probe library(ies) such as cDNA, genomic, BAC, and the like for predominant nucleic acid sequences or additional nucleic acid sequences encoding novel PAAD domain-containing polypeptides. Construction and screening of suitable mammalian cDNA libraries, including human cDNA libraries, is well-known in the art, as demonstrated, for example, in Ausubel et al., supra. Screening of such a cDNA library is initially carried out under low-stringency conditions, which comprise a temperature of less than about 42°C, a formamide concentration of less than about 50%, and a moderate to low salt concentration.

20

Presently preferred probe-based screening conditions comprise a temperature of about 37°C, a formamide concentration of about 20%, and a salt concentration of about 5X standard saline citrate (SSC; 20X SSC contains 3M sodium chloride, 0.3M sodium citrate, pH 7.0). Such conditions will allow the identification of sequences which have a substantial degree of similarity with the probe sequence, without requiring perfect homology. The phrase "substantial similarity" refers to sequences which share at least 50% homology. Hybridization conditions are selected which allow the identification of sequences having at least 70% homology with the probe, while discriminating against sequences which have a lower degree of homology with the probe. As a result, nucleic acids having substantially the same

35

nucleotide sequence as SEQ ID NOs:15, 17, 19, 21, 23, 25 or 27, are obtained.

As used herein, a nucleic acid "probe" is
5 single-stranded nucleic acid, or analog thereof, that has
a sequence of nucleotides that includes at least 15, at
least at least 17, at least 20, at least 22, at least 25,
at least 30, at least 40, at least 50, at least 75, at
least 100, at least 200, at least 300, at least 400, or
10 at least 500 contiguous bases that are substantially the
same as, or the complement of, any contiguous bases set
forth in any of SEQ ID NOs:15, 17, 19, 21, 23, 25 or 27.
Preferred regions from which to construct probes include
5' and/or 3' coding regions of SEQ ID NOs:15, 17, 19, 21,
15 23, 25 or 27. In addition, the entire cDNA encoding
region of an invention PAAD domain-containing
polypeptide, or an entire sequence substantially the same
as SEQ ID NOs:15, 17, 19, 21, 23, 25 or 27, may be used
as a probe. Probes can be labeled by methods well-known
20 in the art, as described hereinafter, and used in various
diagnostic kits.

The invention additionally provides an
oligonucleotide comprising at least 15 contiguous
25 nucleotides of SEQ ID NOs:15, 17, 19, 21, 23, 25 or 27,
or the anti-sense strand thereof. As used herein, the
term "oligonucleotide" refers to a nucleic acid molecule
that includes at least 15 contiguous nucleotides from a
reference nucleotide sequence, can include at least 16,
30 17, 18, 19, 20 21, 22, or at least 25 contiguous
nucleotides, and often includes at least 30, 40, 50, 60,
70, 80, 90, 100, 125, 150, 175, 200, 225, 250, 275, 300,
325, 350, 400, 500, 600, 700 or more contiguous
nucleotides from the reference nucleotide sequence. The
35 reference nucleotide sequence can be the sense strand or
the anti-sense strand.

The oligonucleotides of the invention that contain at least 15 contiguous nucleotides of a reference PAAD domain encoding nucleotide sequence are able to hybridize to PAAD domain encoding nucleotide sequences under moderately stringent hybridization conditions and thus can be advantageously used, for example, as probes to detect PAAD domain encoding DNA or RNA in a sample, and to detect splice variants thereof; as sequencing or PCR primers; as antisense reagents to block transcription of PAAD domain encoding RNA in cells; or in other applications known to those skilled in the art in which hybridization to a PAAD domain encoding nucleic acid molecule is desirable.

15 In accordance with another embodiment of the invention, a method is provided for identifying nucleic acids encoding a PAAD-containing polypeptide, comprising: contacting a sample containing nucleic acids with an invention probe or an invention oligonucleotide, wherein said contacting is effected under high stringency hybridization conditions, and identifying nucleic acids which hybridize thereto. Methods for identification of nucleic acids encoding a PAAD domain-containing polypeptide are disclosed herein.

25 Also provided in accordance with present invention is a method for identifying a PAAD domain encoding nucleotide sequence comprising the steps of using a PAAD domain encoding nucleotide sequence selected from SEQ ID NOS:15, 17, 19, 21, 23, 25 or 27, to identify a candidate PAAD domain encoding nucleotide sequence and verifying the candidate PAAD domain encoding nucleotide sequence by aligning the candidate sequence with known PAAD domain encoding nucleotide sequences, where a conserved PAAD domain sequence or a predicted three dimensional polypeptide structure similar to a known PAAD

domain three dimensional structure confirms the candidate sequence as a PAAD domain encoding sequence. Methods for identifying PAAD-encoding sequences are provided herein (See Examples 1.0, 2.0, 3.0 and 4.0).

5

It is understood that a PAAD domain encoding nucleic acid molecule of the invention, as used herein, specifically excludes previously known nucleic acid molecules consisting of nucleotide sequences having exact
10 sequence identity with the PAAD domain encoding nucleotide sequence (SEQ ID NOS:15, 17, 19, 21, 23, 25 or 27), such as Expressed Sequence Tags (ESTs), Sequence Tagged Sites (STSs) and genomic fragments, deposited in public databases such as the nr, dbest, dbsts, gss and
15 htgs databases, which are available for searching at <http://www.ncbi.nlm.nih.gov/blast/>.

In particular, invention PAAD domain encoding nucleic acid molecules, and PAAD domain-containing
20 polypeptides, excludes the exact, specific and complete nucleic acid and/or amino acid sequences corresponding to any of the nucleotide and/or amino acid sequences having the Genbank (gb), NCBI, EMBL (emb) or DDBJ (dbj) accession numbers described below. Accession numbers
25 specifically excluded include NCBI Accession Nos: GI 4557743, 5094556, 7019331, 7689912, 7020664, 7382417, 2335202, 7690109, 8099799, 8655944, 7662386, 5902751, 2833279, 6523868, 3483677, 10440263, 14731965, 2335202, 15488764, 202805, 9211204, 3483677, 15488878, 14779455,
30 14779445, 14488058, 11096298, 9802275, 9863861, 9863863, 10835255, 10801601, 7020146, 14779447, 13325315, 15215377, 11230601, 9937751, 14758026, 15193291, 13182796, 14731965, 14731967, 4757727, 3341995, 10440263, 14253110, 9153913, and 1383656.

35

Since one of skill in the art will realize that the above-recited excluded sequences may be revised at a later date, the skilled artisan will recognize that the above-recited sequences are excluded as they stand on the
5 priority date of this application.

The isolated nucleic acid molecules of the invention can be used in a variety of diagnostic and therapeutic applications. For example, the isolated
10 nucleic acid molecules of the invention can be used as probes, as described above; as templates for the recombinant expression of PAAD domain-containing polypeptides; or in screening assays such as two-hybrid assays to identify cellular molecules that bind PAAD
15 domain-containing polypeptides.

Another useful method for producing a PAAD domain encoding nucleic acid molecule of the invention involves amplification of the nucleic acid molecule using
20 PCR and invention oligonucleotides and, optionally, purification of the resulting product by gel electrophoresis. Either PCR or RT-PCR can be used to produce a PAAD domain encoding nucleic acid molecule having any desired nucleotide boundaries. Desired
25 modifications to the nucleic acid sequence can also be introduced by choosing an appropriate oligonucleotide primer with one or more additions, deletions or substitutions. Such nucleic acid molecules can be amplified exponentially starting from as little as a
30 single gene or mRNA copy, from any cell, tissue or species of interest.

The invention thus provides methods for detecting a PAAD domain encoding nucleic acid in a
35 sample. The methods of detecting a PAAD domain encoding nucleic acid in a sample can be either qualitative or

quantitative, as desired. For example, the presence, abundance, integrity or structure of a PAAD domain encoding nucleic acid can be determined, as desired, depending on the assay format and the probe used for
5 hybridization or primer pair chosen for application.

Useful assays for detecting a PAAD domain-containing nucleic acid based on specific hybridization with an isolated invention oligonucleotide are well known
10 in the art and include, for example, *in situ* hybridization, which can be used to detect altered chromosomal location of the nucleic acid molecule, altered gene copy number, and RNA abundance, depending on the assay format used. Other hybridization assays
15 include, for example, Northern blots and RNase protection assays, which can be used to determine the abundance and integrity of different RNA splice variants, and Southern blots, which can be used to determine the copy number and integrity of DNA. A hybridization probe can be labeled
20 with any suitable detectable moiety, such as a radioisotope, fluorochrome, chemiluminescent marker, biotin, or other detectable moiety known in the art that is detectable by analytical methods.

25 Useful assays for detecting a PAAD domain encoding nucleic acid in a sample based on amplifying a PAAD domain encoding nucleic acid with two or more invention oligonucleotides are also well known in the art, and include, for example, qualitative or
30 quantitative polymerase chain reaction (PCR); reverse-transcription PCR (RT-PCR); single strand conformational polymorphism (SSCP) analysis, which can readily identify a single point mutation in DNA based on differences in the secondary structure of single-strand DNA that produce
35 an altered electrophoretic mobility upon non-denaturing gel electrophoresis; and coupled PCR, transcription and

translation assays, such as a protein truncation test, in which a mutation in DNA is determined by an altered protein product on an electrophoresis gel. Additionally, the amplified PAAD domain encoding nucleic acid can be
5 sequenced to detect mutations and mutational hot-spots, and specific assays for large-scale screening of samples to identify such mutations can be developed.

In a particular embodiment, a PAAD domain-
10 containing polypeptide, or functional fragment thereof, can be administered to an individual so that the PAAD domain-containing polypeptide or functional fragment is targeted to a tumor to induce apoptosis, inhibit cell proliferation, or otherwise function as a tumor
15 suppressor. One method of delivering a PAAD domain-containing polypeptide to an intracellular target is to fuse a PAAD domain-containing polypeptide or functional fragment to an intracellular-targeting peptide that can penetrate the cell membrane or otherwise deliver a
20 polypeptide to the intracellular environment such as via internalization, thereby causing the fused PAAD domain-containing polypeptide to enter the cell. One example of such an intracellular-targeting peptides is a fusion to the transduction domain of HIV TAT, which allows
25 transduction of up to 100% of cells (Schwarze et al., Science 285:1569-1572 (1999); Vocero-Akbani et al., Nature Med. 5:29-33 (1999)).

Another example of such an intracellular-
30 targeting peptide is the Antennapeida homeoprotein internalization domain (Holinger et al., J. Biol. Chem. 274:13298-13304 (1999)). Still another intracellular-targeting peptide is a peptide that is specific for a cell surface receptor, which allows binding and
35 internalization of a fusion polypeptide via receptor-mediated endocytosis (Ellerby et al., Nature Med. 5:1032-

1038 (1999)). Such intracellular-targeting peptides that mediate specific receptor interactions can be advantageously used to target a tumor (see Ellerby et al., supra, 1999). Alternatively, a PAAD domain-
5 containing polypeptide of the invention can be incorporated, if desired, into liposomes, microspheres or other polymer matrices (Gregoriadis, Liposome Technology, Vols. I to III, 2nd ed., CRC Press, Boca Raton FL (1993)).

10

Also provided are antisense-nucleic acids having a sequence capable of binding specifically with full-length or any portion of an mRNA that encodes PAAD domain-containing polypeptides so as to prevent
15 translation of the mRNA. The antisense-nucleic acid can have a sequence capable of binding specifically with any portion of the sequence of the cDNA encoding PAAD domain-containing polypeptides. As used herein, the phrase "binding specifically" encompasses the ability of a
20 nucleic acid sequence to recognize a complementary nucleic acid sequence and to form double-helical segments therewith via the formation of hydrogen bonds between the complementary base pairs. An example of an antisense-nucleic acid is an antisense-nucleic acid comprising
25 chemical analogs of nucleotides.

Also provided are double-stranded RNA molecules for use in RNA interference methods. RNA interference (RNAi) is a process of sequence-specific gene silencing
30 by post-transcriptional RNA degradation, which is initiated by double-stranded RNA (dsRNA) homologous in sequence to the silenced gene. A suitable double-stranded RNA (dsRNA) for RNAi contains sense and antisense strands of about 21 contiguous nucleotides
35 corresponding to the gene to be targeted that form 19 RNA base pairs, leaving overhangs of two nucleotides at each

3' end (Elbashir et al., Nature 411:494-498 (2001); Bass, Nature 411:428-429 (2001); Zamore, Nat. Struct. Biol. 8:746-750 (2001)). dsRNAs of about 25-30 nucleotides have also been used successfully for RNAi (Karabinos et al., Proc. Natl. Acad. Sci. 98:7863-7868 (2001)). dsRNA can be synthesized in vitro and introduced into a cell by methods known in the art. By such methods, translation of the target polypeptide can be decreased.

10 The present invention provides a method of reducing levels of expression of PAAD domain-containing polypeptides by introducing into a cell anti-sense nucleic acids that inhibit translation or degrade mRNA encoding these polypeptides. Such nucleic acid molecules
15 are designed to recognize and selectively bind to mRNA, such as to mRNA comprising SEQ ID NOs:15, 17, 19, 21, 23, 25 or 27, and are complementary to portions thereof.

 The present invention also provides a method of
20 reducing levels of expression of PAAD domain-containing polypeptides by introducing into a cell dsRNA that degrades mRNA encoding such polypeptides. Such dsRNA contains short contiguous sequences of about 21-30 nucleotides of SEQ ID NOs:15, 17, 19, 21, 23, 25 or 27,
25 and about 21-30 nucleotides complementary thereto, designed such that there is about a 2 base overhang at each 3' end of the double-stranded sequence.

 Compositions comprising an amount of the
30 antisense-nucleic acid or dsRNA effective to reduce expression of PAAD domain-containing polypeptides can further contain an acceptable hydrophobic carrier capable of passing through a cell membrane are also provided herein. Suitable hydrophobic carriers are described, for
35 example, in U.S. Patent Nos. 5,334,761; 4,889,953; 4,897,355, and the like. The acceptable hydrophobic

carrier capable of passing through cell membranes may also comprise a structure which binds to a receptor specific for a selected cell type and is thereby taken up by cells of the selected cell type. For example, the
5 structure can be part of a protein known to bind to a cell-type specific receptor.

The invention also provides a method for expression of a PAAD domain-containing polypeptide by
10 culturing cells containing a PAAD domain encoding nucleic acid under conditions suitable for expression of a PAAD domain-containing polypeptide. Thus, there is provided a method for the recombinant production of a PAAD domain-containing polypeptide of the invention by expressing the
15 PAAD domain encoding nucleic acid sequences in suitable host cells. Recombinant DNA expression systems that are suitable to produce a PAAD domain-containing polypeptide described herein are well-known in the art (see, for example, Ausubel et al., supra (2000)). For example, the
20 above-described nucleotide sequences can be incorporated into vectors for further manipulation. As used herein, a vector refers to a recombinant DNA or RNA plasmid or virus containing discrete elements that are used to introduce heterologous DNA into cells for either
25 expression or replication thereof.

The invention also provides vectors containing the PAAD domain encoding nucleic acids of the invention. Suitable expression vectors are well-known in the art and
30 include vectors capable of expressing nucleic acid operatively linked to a regulatory sequence or element such as a promoter region or enhancer region that is capable of regulating expression of such nucleic acid. Appropriate expression vectors include those that are
35 replicable in eukaryotic cells and/or prokaryotic cells

and those that remain episomal or those which integrate into the host cell genome.

Promoters or enhancers, depending upon the
5 nature of the regulation, can be constitutive or regulated. The regulatory sequences or regulatory elements are operatively linked to a nucleic acid of the invention such that the physical and functional relationship between the nucleic acid and the regulatory
10 sequence allows transcription of the nucleic acid.

Suitable vectors for expression in prokaryotic or eukaryotic cells are well known to those skilled in the art (see, for example, Ausubel et al., supra (2000)).
15 Vectors useful for expression in eukaryotic cells can include, for example, regulatory elements including the SV40 early promoter, the cytomegalovirus (CMV) promoter, the mouse mammary tumor virus (MMTV) steroid-inducible promoter, Moloney murine leukemia virus (MMLV) promoter,
20 and the like. The vectors of the invention are useful for subcloning and amplifying a PAAD domain encoding nucleic acid molecule and for recombinantly expressing a PAAD domain-containing polypeptide. A vector of the invention can include, for example, viral vectors such as
25 a bacteriophage, a baculovirus or a retrovirus; cosmids or plasmids; and, particularly for cloning large nucleic acid molecules, bacterial artificial chromosome vectors (BACs) and yeast artificial chromosome vectors (YACs). Such vectors are commercially available, and their uses
30 are well known in the art. One skilled in the art will know or can readily determine an appropriate promoter for expression in a particular host cell.

The invention additionally provides recombinant
35 cells containing PAAD domain encoding nucleic acids of the invention. The recombinant cells are generated by

introducing into a host cell a vector containing a PAAD domain encoding nucleic acid molecule. The recombinant cells are transduced, transfected or otherwise genetically modified. Exemplary host cells that can be used to express recombinant PAAD molecules include mammalian primary cells; established mammalian cell lines, such as COS, CHO, HeLa, NIH3T3, HEK 293 and PC12 cells; amphibian cells, such as *Xenopus* embryos and oocytes and other vertebrate cells. Exemplary host cells also include insect cells such as *Drosophila*, yeast cells such as *Saccharomyces cerevisiae*, *Saccharomyces pombe*, or *Pichia pastoris*, and prokaryotic cells such as *Escherichia coli*. Additional host cells can be obtained, for example, from ATCC (Manassas, VA)

In one embodiment, PAAD domain encoding nucleic acids can be delivered into mammalian cells, either *in vivo* or *in vitro* using suitable vectors well-known in the art. Suitable vectors for delivering a PAAD domain-containing polypeptide, or a functional fragment thereof to a mammalian cell, include viral vectors such as retroviral vectors, adenovirus, adeno-associated virus, lentivirus, herpesvirus, as well as non-viral vectors such as plasmid vectors. Such vectors are useful for providing therapeutic amounts of a PAAD domain-containing polypeptide (see, for example, U.S. Patent No. 5,399,346, issued March 21, 1995). Delivery of PAAD polypeptides or nucleic acids therapeutically can be particularly useful when targeted to a tumor cell, thereby inducing apoptosis in tumor cells. In addition, where it is desirable to limit or reduce the *in vivo* expression of a PAAD domain-containing polypeptide, the introduction of the antisense strand of the invention nucleic acid is contemplated.

The invention additionally provides an isolated anti-PAAD domain antibody (also referred to herein as an

anti-PAAD antibody) having specific reactivity with a invention PAAD domain-containing polypeptide. The anti-PAAD antibody can be a monoclonal antibody or a polyclonal antibody. The invention further provides cell
5 lines producing monoclonal antibodies having specific reactivity with an invention PAAD domain-containing protien.

The invention thus provides antibodies that
10 specifically bind a PAAD domain-containing polypeptide. As used herein, the term "antibody" is used in its broadest sense to include polyclonal and monoclonal antibodies, as well as antigen binding fragments of such antibodies. With regard to an anti-PAAD antibody of the
15 invention, the term "antigen" means a native or synthesized PAAD domain-containing polypeptide or fragment thereof. An anti-PAAD antibody, or antigen binding fragment of such an antibody, is characterized by having specific binding activity for a PAAD polypeptide
20 or a peptide portion thereof of at least about $1 \times 10^5 \text{ M}^{-1}$. Thus, Fab, F(ab')₂, Fd and Fv fragments of an anti-PAAD antibody, which retain specific binding activity for a PAAD domain-containing polypeptide, are included within the definition of an antibody. Specific
25 binding activity of a PAAD domain-containing polypeptide can be readily determined by one skilled in the art, for example, by comparing the binding activity of an anti-PAAD antibody to a PAAD domain-containing polypeptide versus a reference polypeptide that is not a PAAD domain-
30 containing polypeptide. Methods of preparing polyclonal or monoclonal antibodies are well known to those skilled in the art (see, for example, Harlow and Lane, Antibodies: A Laboratory Manual, Cold Spring Harbor Laboratory Press (1988)).

In addition, the term "antibody" as used herein includes naturally occurring antibodies as well as non-naturally occurring antibodies, including, for example, single chain antibodies, chimeric, bifunctional and humanized antibodies, as well as antigen-binding fragments thereof. Such non-naturally occurring antibodies can be constructed using solid phase peptide synthesis, can be produced recombinantly or can be obtained, for example, by screening combinatorial libraries consisting of variable heavy chains and variable light chains as described by Huse et al., Science 246:1275-1281 (1989)). These and other methods of making, for example, chimeric, humanized, CDR-grafted, single chain, and bifunctional antibodies are well known to those skilled in the art (Winter and Harris, Immunol. Today 14:243-246 (1993); Ward et al., Nature 341:544-546 (1989) ; Harlow and Lane, supra, 1988); Hilyard et al., Protein Engineering: A practical approach (IRL Press 1992); Borrabeck, Antibody Engineering, 2d ed. (Oxford University Press 1995)).

Anti-PAAD antibodies can be raised using a PAAD immunogen such as an isolated PAAD domain-containing functional fragment comprising an amino acid consensus sequence selected from the group consisting of:

- KFKX₁X₂L- (SEQ ID NO:29);
- KLKX₁X₂L- (SEQ ID NO:30);
- RFRX₁X₂L- (SEQ ID NO:31);
- RFXK₁X₂L- (SEQ ID NO:32);
- KFRX₁X₂L- (SEQ ID NO:33); and
- KFKX₁X₂I- (SEQ ID NO:34);

where X₁ and X₂ can be any amino acid; or PAAD domain-containing protein having substantially the same amino acid sequence as SEQ ID NOS:16, 18, 20, 22, 24, 26 or 28, or a portion thereof, which can be prepared from natural

sources or produced recombinantly. Such a portion of a PAAD domain-containing polypeptide is a functional antigenic portion if the antigenic peptides can be used to generate a PAAD domain-containing polypeptide-specific
5 antibody.

The invention further provides a method for detecting the presence of a human PAAD domain-containing polypeptide in a sample by contacting a sample with a
10 PAAD domain specific antibody, and detecting the presence of specific binding of the antibody to the sample, thereby detecting the presence of a human PAAD domain-containing polypeptide in the sample. PAAD domain specific antibodies can be used in diagnostic methods and
15 systems to detect the level of PAAD domain-containing polypeptide present in a sample. As used herein, the term "sample" is intended to mean any biological fluid, cell, tissue, organ or portion thereof, that includes or potentially includes PAAD domain encoding nucleic acids
20 or PAAD domain-containing polypeptides. The term includes samples present in an individual as well as samples obtained or derived from the individual. For example, a sample can be a histologic section of a specimen obtained by biopsy, or cells that are placed in
25 or adapted to tissue culture. A sample further can be a subcellular fraction or extract, or a crude or substantially pure nucleic acid or polypeptide preparation.

30 PAAD domain specific antibodies can also be used for the immunoaffinity or affinity chromatography purification of an invention PAAD domain-containing polypeptide. In addition, methods are contemplated herein for detecting the presence of an invention PAAD
35 domain-containing polypeptide in a cell, comprising contacting the cell with an antibody that specifically

- binds to PAAD domain-containing polypeptides under conditions permitting binding of the antibody to the PAAD domain-containing polypeptides, detecting the presence of the antibody bound to the PAAD domain-containing
- 5 polypeptide, and thereby detecting the presence of invention polypeptides in a cell. With respect to the detection of such polypeptides, the antibodies can be used for *in vitro* diagnostic or *in vivo* imaging methods.
- 10 Immunological procedures useful for *in vitro* detection of target PAAD domain-containing polypeptides in a sample include immunoassays that employ a detectable antibody. Such immunoassays include, for example, immunohistochemistry, immunofluorescence, ELISA assays,
- 15 radioimmunoassay, FACS analysis, immunoprecipitation, immunoblot analysis, Pandex microfluorimetric assay, agglutination assays, flow cytometry and serum diagnostic assays, which are well known in the art (Harlow and Lane, supra (1988); Harlow and Lane, Using Antibodies: A
- 20 Laboratory Manual, Cold Spring Harbor Press (1999)).

- An antibody can be made detectable by various means well known in the art. For example, a detectable marker can be directly attached to the antibody or
- 25 indirectly attached using, for example, a secondary agent that recognizes the PAAD specific antibody. Useful markers include, for example, radionucleotides, enzymes, binding proteins such as biotin, fluorogens, chromogens, fluorescent labels and chemiluminescent labels. A
- 30 description of immunofluorescent analytic techniques is found in DeLuca, "Immunofluorescence Analysis", in Antibody As a Tool, Marchalonis et al., eds., John Wiley & Sons, Ltd., pp. 189-231 (1982), which is incorporated herein by reference.

In addition to detecting the presence of a PAAD domain-containing polypeptide, invention anti-PAAD antibodies are contemplated for use herein to alter the activity of the PAAD domain-containing polypeptide in living animals, in humans, or in biological tissues or fluids isolated therefrom. The term "alter" refers to the ability of a compound such as a PAAD domain-containing polypeptide, a PAAD domain encoding nucleic acid, an agent or other compound to increase or decrease biological activity which is modulated by the compound, by functioning as an agonist or antagonist of the compound. Accordingly, compositions comprising a carrier and an amount of an antibody having specificity for PAAD domain-containing polypeptides effective to block naturally occurring ligands or other PAAD-associated polypeptides from binding to invention PAAD domain-containing polypeptides are contemplated herein. For example, a monoclonal antibody directed to an epitope of an invention PAAD domain-containing polypeptide, including an amino acid sequence substantially the same as SEQ ID NOS:16, 18, 20, 22, 24, 26 or 28, can be useful for this purpose.

The present invention further provides transgenic non-human mammals that are capable of expressing exogenous nucleic acids encoding PAAD domain-containing polypeptides. As employed herein, the phrase "exogenous nucleic acid" refers to nucleic acid sequence which is not native to the host, or which is present in the host in other than its native environment, for example, as part of a genetically engineered DNA construct. In addition to naturally occurring PAAD domain-containing polypeptide levels, a PAAD domain-containing polypeptide of the invention can either be overexpressed or underexpressed in transgenic mammals, for example, underexpressed in a knock-out animal.

Animal model systems useful for elucidating the physiological and behavioral roles of PAAD domain-containing polypeptides are also provided, and are produced by creating transgenic animals in which the

5 expression of the PAAD domain-containing polypeptide is altered using a variety of techniques. Examples of such techniques include the insertion of normal or mutant versions of nucleic acids encoding a PAAD domain-containing polypeptide by microinjection, retroviral

10 infection or other means well known to those skilled in the art, into appropriate fertilized embryos to produce a transgenic animal, see, for example, Hogan et al., Manipulating the Mouse Embryo: A Laboratory Manual (Cold Spring Harbor Laboratory, (1986)). Transgenic animal

15 model systems are useful for *in vivo* screening of compounds for identification of specific ligands, such as agonists or antagonists, which activate or inhibit a biological activity.

20 In accordance with another embodiment of the invention, a method is provided for identifying a PAAD-associated polypeptide (PAP). The method is carried out by contacting an invention PAAD domain-containing polypeptide with a candidate PAP and detecting

25 association of the PAAD domain-containing polypeptide with the PAP.

As used herein, the term "PAAD-associated polypeptide" or "PAP" means a polypeptide that can

30 specifically bind to the PAAD domain-containing polypeptides of the invention, or to any functional fragment of a PAAD domain-containing polypeptide of the invention. Because PAAD domain-containing polypeptides of the invention contain domains which can self-

35 associate, PAAD domain-containing polypeptides are encompassed by the term PAP. An exemplary PAP is a

protein or a polypeptide portion of a protein that can bind a PAAD, NB-ARC, LRR or ANGIO-R domain of an invention PAAD domain-containing polypeptide. A PAP can be identified, for example, using *in vitro* or *in vivo*

5 protein-interaction assays and methods known in the art, including yeast two-hybrid assays, co-immunoprecipitation, GST fusion co-purification, GST pull-down assays and the like (see, for example, Ausubel et al., supra (2000)). Additional methods include, for

10 example, scintillation proximity assay (SPA) (Alouani, *Methods Mol. Biol.* 138:135-41 (2000)), UV or chemical cross-linking (Fancy, Curr. Opin. Chem. Biol. 4:28-33 (2000)), competition binding assays (Yamamura et al., Methods in Neurotransmitter Receptor Analysis, Raven

15 Press, New York, 1990), biomolecular interaction analysis (BIA) such as surface plasmon resonance (SPR) (Weinberger et al., Pharmacogenomics 1:395-416 (2000)), mass spectrometry (MS) (McLafferty et al., Science 284:1289-1290 (1999) and Degterev, et al., Nature Cell Biology

20 3:173-182 (2001)), nuclear magnetic resonance (NMR) (Shuker et al., Science 274:1531-1534 (1996), Hajduk et al., J. Med. Chem. 42:2315-2317 (1999), and Chen and Shapiro, Anal. Chem. 71:669A-675A (1999)), and fluorescence polarization assays (FPA) (Degterev et al.,

25 supra, 2001).

Exemplary PAPs contemplated herein can include a protein involved in regulating apoptosis, caspase activation or NFkB induction, and other PAAD domain-

30 containing polypeptides, selected from: Apaf-1, CED4, Nod1/CARD4, ASC-1, CARDX1, pro-Casp1, pro-Casp2, pro-Casp4, pro-Casp5, pro-Casp7, pro-Casp11, pro-Casp12, pro-Casp14, CED3, Dronc, Raidd/CRADD, Cardiak (RIP2, Rick), Bcl-1/CIPER, ARC, NOP30, cIAP-1, cIAP-2, Fadd/mort1, pro-

35 Casp8, pro-Casp10, Dredd, c-Flip/flame, KSV/V-Flip, MCV, DEDD/DEFT, PEA-15, Flash, BAP31, BAR, RIP, IRAK-1, IRAK-

2, IRAK-M, My D88, NMP-84, Ankyrin-1, Ankyrin-3, TNFR1, NGFR, Fas, DR3, DR4, DR5, DR6, Tradd, Fadd, Raidd2, DAP Kinase, NIK, IKK α , IKK β , I κ B, p65, p50, IKAP, pyrin, pyrin2, PAN1, PAN2, PAN3, PAN4, PAN5, PAN6, ASC, ASC2, 5 NAC, AIM2, IFI16, MO13L, p52, p100, p105, ParaCaspase (MALT1) and all members of the NF κ B/I κ B families. The naturally occurring sequences of these molecules from a variety of species, including human and rodent, are well known in the art. The skilled person can readily 10 determine fragments and modifications of naturally occurring PAP sequences that retain their ability to associate with a PAAD domain-containing polypeptide, or domain therefrom, in the assays described herein.

15 As disclosed herein, exemplary PAPs that associate with ASC include ASC, ASC2, Caspase-1, Card10, Nod1, Cardiak, NIK and IKK-i. An exemplary PAP that associates with PAN2 is I κ B α . An exemplary PAP that associates with PAN6 is IKAP.

20 The normal association between a PAAD domain-containing polypeptide and a PAP polypeptide in a cell can be altered due, for example, to the expression in the cell of a variant PAP or PAAD domain-containing 25 polypeptide, respectively, either of which can compete with the normal binding function of a PAAD domain-containing polypeptide and, therefore, can decrease the association of PAP and PAAD domain-containing polypeptides in a cell. The term "variant" is used 30 generally herein to mean a polypeptide that is different from the PAP or PAAD domain-containing polypeptide that normally is found in a particular cell type. Thus, a variant can include a mutated protein or a naturally occurring protein, such as an isoform, that is not 35 normally found in a particular cell type.

PAAD domain-containing polypeptides and PAAD-associated polypeptides of the invention can be characterized, for example, using *in vitro* binding assays or the yeast two hybrid system. An *in vivo* transcription activation assay such as the yeast two hybrid system is particularly useful for identifying and manipulating the association of proteins. In addition, the results observed in such an assay likely mirror the events that naturally occur in a cell. Thus, the results obtained in such an *in vivo* assay can be predictive of results that can occur in a cell in a subject such as a human subject.

A transcription activation assay such as the yeast two hybrid system is based on the modular nature of transcription factors, which consist of functionally separable DNA-binding and trans-activation domains. When expressed as separate proteins, these two domains fail to mediate gene transcription. However, transcription activation activity can be restored if the DNA-binding domain and the trans-activation domain are bridged together due, for example, to the association of two proteins. The DNA-binding domain and trans-activation domain can be bridged, for example, by expressing the DNA-binding domain and trans-activation domain as fusion proteins (hybrids), provided that the proteins that are fused to the domains can associate with each other. The non-covalent bridging of the two hybrids brings the DNA-binding and trans-activation domains together and creates a transcriptionally competent complex. The association of the proteins is determined by observing transcriptional activation of a reporter gene.

The yeast two hybrid systems exemplified herein use various strains of *S. cerevisiae* as host cells for vectors that express the hybrid proteins. A

transcription activation assay also can be performed using, for example, mammalian cells. However, the yeast two hybrid system is particularly useful due to the ease of working with yeast and the speed with which the assay
5 can be performed. For example, yeast host cells containing a lacZ reporter gene linked to a LexA operator sequence can be used to demonstrate that a PAAD domain of an invention PAAD domain-containing polypeptide can interact with itself or other PAAD domain-containing
10 polypeptides. For example, the DNA-binding domain can consist of the LexA DNA-binding domain, which binds the LexA promoter, fused to the PAAD domain of a PAAD domain-containing polypeptide of the invention and the trans-activation domain can consist of the B42 acidic
15 region separately fused to several cDNA sequences which encode known PAAD domain-containing polypeptides. When the LexA domain is non-covalently bridged to a trans-activation domain fused to a PAAD domain-containing polypeptide, the association can activate transcription
20 of the reporter gene.

A PAP, for example, a PAAD domain-containing polypeptide, a CARD-containing polypeptide, an NB-ARC-containing polypeptide or a LRR-containing
25 polypeptide, also can be identified using well known *in vitro* assays, for example, an assay utilizing a glutathione-S-transferase (GST) fusion protein. Such an *in vitro* assay provides a simple, rapid and inexpensive method for identifying and isolating a PAP. Such an *in*
30 *vitro* assay is particularly useful in confirming results obtained *in vivo* and can be used to characterize specific binding domains of a PAP. For example, a GST can be fused to a PAAD domain-containing polypeptide of the invention, and expressed and purified by binding to an
35 affinity matrix containing immobilized glutathione. If

desired, a sample that can contains a PAP or active fragments of a PAP can be passed over an affinity column containing bound GST/PAAD and a PAP that binds to a PAAD domain-containing polypeptide can be obtained. In
5 addition, GST/PAAD can be used to screen a cDNA expression library, wherein binding of the GST/PAAD fusion protein to a clone indicates that the clone contains a cDNA encoding a PAP.

10 Thus, one of skill in the art will recognize that using the PAAD domain-containing polypeptides described herein, a variety of methods, such as protein purification, protein interaction cloning, or protein mass-spectrometry, can be used to identify a PAP.

15 Although the term "PAP" is used generally, it should be recognized that a PAP that is identified using the novel polypeptides described herein can be a fragment of a protein. Thus, as used herein, a PAP also includes
20 a polypeptide that specifically associates to a portion of an invention PAAD domain-containing polypeptide that does not include a PAAD domain. For example, a PAP can associate with the NB-ARC domain of an invention PAN. As used herein, a "candidate PAP" refers to a polypeptide
25 containing a polypeptide sequence know or suspected of binding one or more PAAD domain-containing polypeptides of the invention. Thus, a PAP can represent a full-length protein or a PAAD-associating fragment thereof. Since a PAP polypeptide can be a full-length protein or a
30 PAAD-associating fragment thereof, one of skill in the art will recognize that a PAP-encoding nucleic acid, such as the genomic sequence, an mRNA sequence or a cDNA sequence need not encode the full-length protein. Thus, a cDNA can encode a polypeptide that is a fragment of a
35 full-length PAP which, nevertheless, binds one or more

invention PAAD domain-containing polypeptides. It is also within the scope of the invention that a full-length PAP can assume a conformation that does not, absent some post-translational modification, bind a PAAD domain-
5 containing polypeptide of the invention, due, for example, to steric blocking of the binding site. Thus, a PAP can be a protein or a polypeptide portion of a protein that can bind one of the PAAD domain-containing polypeptides of the invention. Also, it should be
10 recognized that a PAP can be identified by using a minimal polypeptide derived from the sequences of the PAAD domain-containing polypeptides of the invention, and does not necessarily require that the full-length molecules be employed for identifying such PAPs.

15
Since PAAD domain-containing polypeptides can be involved in apoptosis, the association of a PAP with a PAAD domain-containing polypeptide can affect the sensitivity or resistance of a cell to apoptosis or can
20 induce or block apoptosis induced by external or internal stimuli. The identification of various PAPs by use of known methods can be used to determine the function of these PAPs in cell death or signal transduction pathways controlled by PAAD domain-containing polypeptides,
25 allowing for the development of assays that are useful for identifying agents that effectively alter the association of a PAP with a PAAD domain-containing polypeptide. Such agents can be useful for providing effective therapy for conditions caused, at least in
30 part, by insufficient apoptosis, such as cancer, autoimmune disease or certain viral infections. Such agents can also be useful for providing an effective therapy for diseases where excessive apoptosis is known to occur, such as stroke, heart failure, or AIDS; as well
35 as inflammatory diseases, such as inflammatory bowel

diseases (e.g. Crohn's disease and ulcerative colitus);
rheumatoid arthritis, sepsis, trauma, allograft rejection
and graft-versus-host disease.

5 Since PAAD domain-containing polypeptides are
also involved in regulating NF κ B activity, the
association of a PAP with a PAAD domain-containing
polypeptide can also affect responses of cells to stimuli
that activate NF κ B transcription, including TNF α and IL-1
10 and other proinflammatory cytokines, T- and B-cell
mitogens, bacteria, bacterial lipopolysaccharide (LPS),
viruses, viral proteins, double stranded RNA, and
physical and chemical stresses. The identification of
various PAPs as described herein and agents that
15 effectively alter the association of a PAP with a PAAD
domain-containing polypeptide can be used to provide
effective therapy for conditions mediated, at least in
part, by NF κ B, including, for example, inflammatory
conditions, infections, cancers, neurodegenerative
20 disorders, arthritis and asthma.

Assays of the invention can be used for
identification of agents that alter the self-association
of the PAAD domain-containing polypeptides of the
25 invention. Thus, the methods of the invention can be
used to identify agents that alter the self-association
of invention PAAD domains, such as SEQ ID NOS:1-14 and
PAAD domain-containing proteins, such as SEQ ID NOs:16,
18, 20, 22, 24, 26 and 28, via their PAAD domains, NB-ARC
30 domains, LRR domains, ANGIO-R domains or other domains
within these polypeptides.

The ATP-binding and hydrolysis of the NB-ARC
domains can be critical for function of a PAAD domain-
35 containing polypeptide, for example, by altering the

oligomerization of the PAAD domain-containing polypeptide. Thus, agents that interfere with or enhance ATP or nucleotide binding and/or hydrolysis by the NB-ARC domain of a PAAD domain-containing polypeptide of the invention, such as invention PAN proteins, can also be useful for altering the activity of these polypeptides in cells.

A further embodiment of the invention provides a method to identify agents that can effectively alter PAAD domain-containing polypeptide activity, for example the ability of PAAD domain-containing polypeptides to associate with one or more heterologous proteins. Thus, the present invention provides a screening assay useful for identifying an effective agent, which can alter the association of a PAAD domain-containing polypeptide, such as a PAN, with a PAAD-associated polypeptide (PAP), such as a heterologous PAAD domain-containing polypeptide.

Effective agents can be useful to alter a biochemical process modulated by a PAAD domain-containing polypeptide of the invention. Additional biochemical processes (also referred to herein as "cell activities") modulated by PAAD domain-containing polypeptide include, for example, apoptosis, regulation of NF κ B induction, cytokine processing, cytokine receptor signaling, cJUN N-terminal kinase induction, caspase-mediated proteolytic activation/inhibition, transcription, inflammation and cell adhesion.

As used herein, the term "agent" means a chemical or biological molecule such as a simple or complex organic molecule, a peptide, a peptido-mimetic, a polypeptide, a protein or an oligonucleotide that has the potential for altering the association of a PAAD domain-

containing polypeptide with a heterologous protein or altering the ability of a PAAD domain-containing polypeptide to self-associate or altering the ligand binding or biological activity of a PAAD domain-

5 containing polypeptide. An exemplary ligand binding activity is nucleotide binding activity, such as ADP or ATP binding activity; and exemplary catalytic activities are nucleotide hydrolytic activity and proteolytic activity. In addition, the term "effective agent" is

10 used herein to mean an agent that is confirmed as capable of altering the association of a PAAD domain-containing polypeptide with a heterologous protein or altering the ability of a PAAD domain-containing polypeptide to self-associate or altering the ligand binding or

15 catalytic activity of a PAAD domain-containing polypeptide. For example, an effective agent may be an anti-PAAD antibody, a PAAD-associated polypeptide and the like.

20 As used herein, the term "alter the association" means that the association between two specifically interacting polypeptides either is increased or decreased due to the presence of an effective agent. As a result of an altered association of PAAD domain-

25 containing polypeptide with another polypeptide in a cell, the activity of the PAAD domain-containing polypeptide or the PAP can be increased or decreased, thereby altering a biochemical process, for example, the level of apoptosis or NFkB transcriptional activity in

30 the cell. As used herein, the term "alter the activity" means that the agent can increase or decrease the activity of a PAAD domain-containing polypeptide in a cell, thereby modulating a biochemical process in a cell, for example, the level of apoptosis or NFkB

35 transcriptional activity in the cell. Similarly, the

term "alter the level" of a biological process modulated by a PAAD domain-containing polypeptide refers to an increase or decrease a biochemical process which occurs upon altering the activity of a PAAD domain-containing
5 polypeptide. For example, an effective agent can increase or decrease the PAAD:PAAD-associating activity of a PAAD domain-containing polypeptide, which can result in altered apoptosis or increased or decreased NFκB transcriptional activity. In another example, alteration
10 of the ATP hydrolysis activity can modulate the ability of the NB-ARC domain of a PAAD domain-containing polypeptide to associate with other NB-ARC-containing polypeptides, such as Apaf-1, thereby altering any process effected by such association between a PAAD
15 domain-containing polypeptide and an NB-ARC-containing polypeptide.

An effective agent can act by interfering with the ability of a PAAD domain-containing polypeptide to
20 associate with another polypeptide, or can act by causing the dissociation of a PAAD domain-containing polypeptide from a complex with a PAAD-associated polypeptide, wherein the ratio of bound PAAD domain-containing polypeptide to free PAAD domain-containing polypeptide is
25 related to the level of a biochemical process, such as apoptosis or NFκB transcriptional activity, in a cell. For example, binding of a ligand to a PAP can allow the PAP, in turn, to bind a specific PAAD domain-containing polypeptide such that all of the specific PAAD domain-
30 containing polypeptide is bound to a PAP.

An effective agent can be useful, for example, to increase the level of apoptosis in a cell such as a cancer cell, which is characterized by having a decreased
35 level of apoptosis as compared to its normal cell

counterpart. An effective agent also can be useful, for example, to decrease the level of apoptosis in a cell such as a T lymphocyte in a subject having a viral disease such as acquired immunodeficiency syndrome, which
5 is characterized by an increased level of apoptosis in an infected T cell as compared to a normal T cell. Thus, an effective agent can be useful as a medicament for altering the level of apoptosis in a subject having a pathology characterized by increased or decreased
10 apoptosis. In addition, an effective agent can be used, for example, to decrease the level of apoptosis and, therefore, increase the survival time of a cell such as a hybridoma cell in culture. The use of an effective agent to prolong the survival of a cell *in vitro* can
15 significantly improve bioproduction yields in industrial tissue culture applications.

An effective agent can also be useful to increase or decrease NF κ B transcriptional activity, and
20 thus can be used to provide effective therapy for conditions mediated, at least in part, by NF κ B, including, for example, inflammatory conditions (e.g. inflammatory bowel diseases, such as Crohn's disease and ulcerative colitus), infections, cancers,
25 neurodegenerative disorders, arthritis, asthma, stroke, heart failure, AIDS, sepsis, trauma, allograft rejection and graft-versus-host disease.

A PAAD domain-containing polypeptide that lacks
30 the ability to bind the CARD domain, NB-ARC domain or LRR domain of another polypeptide but retains the ability to self-associate via its PAAD domain or to bind to other PAAD domain-containing polypeptides is an example of an effective agent, since the expression of a non-NB-ARC-
35 associating or non-catalytically active PAAD domain-

containing polypeptide in a cell can alter the association of a the endogenous PAAD domain-containing polypeptide with itself or with PAPs.

5 Thus, it should be recognized that a mutation of a PAAD domain-containing polypeptide can be an effective agent, depending, for example, on the normal levels of PAAD domain-containing polypeptide and PAAD-associated polypeptide that occur in a particular cell
10 type. In addition, an active fragment of a PAAD domain-containing polypeptide can be an effective agent, provided the active fragment can alter the association of a PAAD domain-containing polypeptide and another polypeptide in a cell. Such active fragments, which can
15 be peptides as small as about five amino acids, can be identified, for example, by screening a peptide library (see, for example, Ladner et al., U.S. Patent No: 5,223,409, which is incorporated herein by reference) to identify peptides that can bind a PAAD-associated
20 polypeptide.

 Similarly, a peptide or polypeptide portion of a PAAD-associated polypeptide also can be an effective agent. A peptide of PAAD-associated polypeptide can be
25 useful, for example, for decreasing the association of a PAAD domain-containing polypeptide with a PAP in a cell by competing for binding to the PAAD domain-containing polypeptide. A non-naturally occurring peptido-mimetic also can be useful as an effective agent. Such a
30 peptido-mimetic can include, for example, a peptoid, which is peptide-like sequence containing N-substituted glycines, or an oligocarbamate. A peptido-mimetic can be particularly useful as an effective agent due, for example, to having an increased stability to enzymatic
35 degradation *in vivo*.

In accordance with another embodiment of the present invention, there is provided a method of identifying an effective agent that alters the association of an invention PAAD domain-containing polypeptide with a PAAD-associated polypeptide (PAP), by the steps of:

(a) contacting the PAAD domain-containing polypeptide and PAP polypeptides, under conditions that allow the PAAD domain-containing polypeptide and PAP polypeptides to associate, with an agent suspected of being able to alter the association of the PAAD domain-containing polypeptide and PAP polypeptides; and

(b) detecting the altered association of the PAAD domain-containing polypeptide and PAP polypeptides, where the altered association identifies an effective agent.

Methods well-known in the art for detecting the altered association of the PAAD domain-containing polypeptide and PAP polypeptides, for example, measuring protein:protein binding, protein degradation or apoptotic activity can be employed in bioassays described herein to identify agents as agonists or antagonists of PAAD domain-containing polypeptides. As described herein, PAAD domain-containing polypeptides have the ability to self-associate. Thus, methods for identifying effective agents that alter the association of a PAAD domain-containing polypeptide with a PAP are useful for identifying effective agents that alter the ability of a PAAD domain-containing polypeptide to self-associate.

As used herein, "conditions that allow said PAAD domain-containing polypeptide and PAP polypeptides

to associate" refers to environmental conditions in which a PAAD domain-containing polypeptide and PAP specifically associate. Such conditions will typically be aqueous conditions, with a pH between 3.0 and 11.0, and
5 temperature below 100°C. Preferably, the conditions will be aqueous conditions with salt concentrations below the equivalent of 1 M NaCl, and pH between 5.0 and 9.0, and temperatures between 0°C and 50°C. Most preferably, the conditions will range from physiological conditions of
10 normal yeast or mammalian cells, or conditions favorable for carrying out *in vitro* assays such as immunoprecipitation and GST protein:protein association assays, and the like.

15 In another embodiment of the invention, a method is provided for identifying agents that modulate a biological activity of an invention PAAD domain-containing polypeptide, such as ligand interaction or catalytic activity. The method contains the steps of
20 contacting an invention PAAD domain-containing polypeptide with an agent suspected of modulating a ligand binding or biological activity of the PAAD domain-containing polypeptide and measuring a biological activity of the PAAD domain-containing polypeptide, where
25 modulated biological activity identifies the agent as an agent that alters the biological activity of a PAAD domain-containing polypeptide.

As used herein in regard to biological
30 activity, "modulate" refers to an increase or decrease in the measured biological activity. Thus, modulation encompasses inhibition of biological activity as well as activation or enhancement of biological activity. Exemplary biological activities include nucleotide

binding, nucleotide hydrolysis and modulation of NF κ B activation.

Methods for measuring ligand binding and other
5 biological activities are well known in the art, as disclosed herein. For example, an agent known or suspected of modulating a biological activity can be contacted with an invention PAAD domain-containing polypeptide in vivo or in vitro, and the activity can be
10 measured using known methods. Exemplary agents that can modulate a biological activity include peptides, peptidomimetics and other peptide analogs, non-peptide organic molecules such as naturally occurring protease inhibitors and derivatives thereof, nucleotides and
15 nucleotide analogs, and the like. Such inhibitors can be either reversible or irreversible, as is well known in the art.

Agents that modulate a biological activity of a
20 PAAD domain-containing polypeptide identified using the invention methods can be used to modulate the activity of a PAAD domain-containing polypeptide. For example, an agent can modulate the nucleotide binding or nucleotide hydrolytic activity of an NB-ARC domain of a PAAD domain-
25 containing polypeptide. In another example, an agent can modulate the NF κ B regulatory activity of the PAAD domain. Methods of modulating a biological activity of invention PAAD domain-containing proteins can be used in methods of altering biochemical processes modulated by PAAD domain-
30 containing proteins, such as the biochemical processes disclosed herein.

In yet another embodiment of the present invention, there are provided methods for altering a

biological activity of a PAAD domain-containing polypeptide of the invention, the method comprising:
contacting an PAAD domain-containing polypeptide with an effective amount of an agent
5 identified by the herein-described bioassays.

The present invention also provides *in vitro* screening assays. Such screening assays are particularly useful in that they can be automated, which allows for
10 high through-put screening, for example, of randomly or rationally designed agents such as drugs, peptidomimetics or peptides in order to identify those agents that effectively alter the association of a PAAD domain-containing polypeptide and a PAP or the catalytic or
15 ligand binding activity of a PAAD domain-containing polypeptide and, thereby, alter a biochemical process modulated by a PAAD domain-containing polypeptide such as apoptosis. An *in vitro* screening assay can utilize, for example, a PAAD domain-containing polypeptide including a
20 PAAD domain-containing fusion protein such as a PAAD-glutathione-S-transferase fusion protein. For use in the *in vitro* screening assay, the PAAD domain-containing polypeptide should have an affinity for a solid substrate as well as the ability to associate with
25 a PAAD-associated polypeptide. For example, when a PAAD domain-containing polypeptide is used in the assay, the solid substrate can contain a covalently attached anti-PAAD antibody. Alternatively, a GST/PAAD fusion protein can be used in the assay and the solid substrate
30 can contain covalently attached glutathione, which is bound by the GST component of the GST/PAAD fusion protein. Similarly, a PAAD-associated polypeptide can be used in any of a variety of *in vitro* enzymatic or *in vitro* binding assays known in the art and described in
35 texts such as Ausubel et al., *supra*, 2000.

An *in vitro* screening assay can be performed by allowing a PAAD domain-containing polypeptide or fragment thereof to bind to the solid support, then adding a PAAD-associated polypeptide and an agent to be tested.

- 5 Reference reactions, which do not contain an agent, can be performed in parallel. Following incubation under suitable conditions, which include, for example, an appropriate buffer concentration and pH and time and temperature that permit binding of the particular PAAD
- 10 domain-containing polypeptide and PAAD-associated polypeptide, the amount of protein that has associated in the absence of an agent and in the presence of an agent can be determined. The association of a PAAD-associated polypeptide with a PAAD domain-containing polypeptide can
- 15 be detected, for example, by attaching a detectable moiety such as a radionuclide or a fluorescent label to a PAAD-associated polypeptide and measuring the amount of label that is associated with the solid support, wherein the amount of label detected indicates the amount of
- 20 association of the PAAD-associated polypeptide with a PAAD domain-containing polypeptide. An effective agent is determined by comparing the amount of specific binding in the presence of an agent as compared to a reference level of binding, wherein an effective agent alters the
- 25 association of PAAD domain-containing polypeptide with the PAAD-associated polypeptide. Such an assay is particularly useful for screening a panel of agents such as a peptide library in order to detect an effective agent.

30

Additionally, a PAAD domain-containing polypeptide or domain thereof, such as a PAAD domain or NB-ARC domain, can be contacted with a candidate agent and association between the polypeptide and the candidate

35 agent determined. Agents that bind in such assays can

further be tested for their ability to alter a biological activity of a PAAD domain-containing polypeptide or for their ability to alter associations between a PAAD domain-containing polypeptide and a PAP.

5

Various binding assays described above, such as the two hybrid assay, co-immunoprecipitation assay, co-localization assay, scintillation proximity assay (SPA), UV or chemical cross-linking, biomolecular interaction analysis (BIA), mass spectrometry (MS), nuclear magnetic resonance (NMR), and fluorescence polarization assays (FPA) can be used to identify an effective agent.

Another assay for screening of agents that alter the activity of a PAAD domain-containing polypeptide is based on altering the phenotype of yeast by expressing a PAAD domain-containing polypeptide. In one embodiment, expression of a PAAD domain-containing polypeptide can be inducible (Tao et al., J. Biol. Chem. 273:23704-23708 (1998), and the compounds can be screened when PAAD domain-containing polypeptide expression is induced. PAAD domain-containing polypeptides of the invention can also be co-expressed in yeast with PAP polypeptides used to screen for compounds that antagonize the activity of the PAAD domain-containing polypeptide.

A biological activity that can potentially be altered by an agent is PAAD domain-mediated modulation of NFkB activity. An agent that increases or decreases PAAD domain-mediated inhibition of NFkB activity with correspondingly decrease or increase NFkB activity. Such agents can be useful for treating conditions associated with decreased or increased NFkB activity as described herein, including, for example, inflammation, autoimmune

diseases, neurodegenerative diseases, cancer and infectious disorders.

The invention thus provides methods of

5 identifying agents that modulate PAAD domain-mediated inhibition or stimulation of NF κ B activity. In one embodiment, a cell that recombinantly expresses a PAAD domain-containing polypeptide is contacted with a candidate agent and altered NF κ B activity, such as

10 increased or decreased activity, is detected in the cell. As NF κ B activity in an unstimulated cell is normally low, such methods can be practiced by contacting the cell with an NF κ B inducer, such as TNF α or IL1 β , or recombinantly expressing within the cell an NF κ B inducer, such as

15 Bcl10, TRAF2, TRAF6, NIK, RIP2, p65, IRAK2, IRAK3, MyD88, RIP, IL-1R, Nod1, IKK α , IKK β , TNFR1, and the like, such that the PAAD domain-containing polypeptide inhibits the induced level of NF κ B activity.

20 The skilled person can employ appropriate controls to confirm that the effect of the candidate agent is specific for the PAAD domain-containing polypeptide. For example, the effect on NF κ B activation of the candidate agent can be compared to the effect in a

25 control cell that does not express nucleic acid molecule encoding a PAAD domain-containing polypeptide. Additionally, the effect of the candidate agent on NF κ B activation can be compared with the effect of a vehicle control not containing the agent.

30

Various methods of determining the amount of NF κ B activity in a cell are well known in the art. For example, binding assays have been developed that take advantage of the observation that active NF κ B, but not

35 inactive NF κ B, binds to DNA. Therefore, the binding of a

test cell extract to a labeled oligonucleotide containing an NFkB consensus binding site can be assayed. Active NFkB in the cell extract is evidenced by retardation of the mobility of the oligonucleotide band on a gel

5 (Schreck et al., Nucleic Acids Res. 18:6497-6502 (1990); Rusher et al., J. Biotech. 78:163-170 (2000)). An alternative method is to attach an oligonucleotide containing an NFkB consensus binding site to a multiwell plate and detect bound, active NFkB in an ELISA-type

10 assay using NFkB antibodies (Renard et al., Nucleic Acids Res. 29:E21 (2001)).

An alternative assay for determining the amount of NFkB activity in a cell monitors the cleavage of the

15 NFkB precursors p100 or p105 to the active p50 or p55 subunits (see, for example, Lin et al., Mol. Cell. Biol. 16:2248-2254 (1996); Morgan et al., Cancer Res. 59:6205-6213 (1999); Uren et al., Mol. Cell 6:961-967 (2000)).

20 Activity assays can also be used to determine the amount of NFkB activity in a cell. For example, a reporter gene such as the luciferase, β -galactosidase or secretory alkaline phosphatase gene can be placed under the control of a promoter containing the NFkB consensus

25 site. NFkB activity in cells transfected with the reporter construct is evidenced by expression of the product of the reporter gene (Moon et al., Anal. Biochem. 292:17-21 (2001); see Examples).

30 Additional methods of monitoring NFkB activation include, for example, monitoring cytoplasmic IxB degradation using antibodies directed against IxB (Sun et al., Proc. Natl. Acad. Sci. USA 91:1346-1350 (1994), and monitoring exposure of the nuclear

35 localization signal (NLS) of active NFkB using NLS-

specific antibodies (Zabel et al., EMBO J. 12:201-211 (1993)).

Also provided with the present invention are
5 assays to identify agents that alter PAAD domain-
containing polypeptide expression. Methods to determine
PAAD domain-containing polypeptide expression can involve
detecting a change in PAAD domain-containing polypeptide
abundance in response to contacting the cell with an
10 agent that modulates PAAD domain-containing polypeptide
expression. Assays for detecting changes in polypeptide
expression include, for example, immunoassays with PAAD
domain specific antibodies, such as immunoblotting,
immunofluorescence, immunohistochemistry and
15 immunoprecipitation assays, as described herein.

As understood by those of skill in the art,
assay methods for identifying agents that alter PAAD
domain-containing polypeptide activity generally require
20 comparison to a reference. One type of a "reference" is
a cell or culture that is treated substantially the same
as the test cell or test culture exposed to the agent,
with the distinction that the "reference" cell or culture
is not exposed to the agent. Another type of "reference"
25 cell or culture can be a cell or culture that is
identical to the test cells, with the exception that the
"reference" cells or culture do not express a PAAD
domain-containing polypeptide. Accordingly, the response
of the transfected cell to an agent is compared to the
30 response, or lack thereof, of the "reference" cell or
culture to the same agent under the same reaction
conditions.

Methods for producing pluralities of agents to use in screening for compounds that alter the activity of a PAAD domain-containing polypeptide, including chemical or biological molecules such as simple or complex organic molecules, metal-containing compounds, carbohydrates, peptides, proteins, peptidomimetics, glycoproteins, lipoproteins, nucleic acids, antibodies, and the like, are well known in the art and are described, for example, in Huse, U.S. Patent No. 5,264,563; Francis et al., Curr. Opin. Chem. Biol. 2:422-428 (1998); Tietze et al., Curr. Biol., 2:363-371 (1998); Sofia, Mol. Divers. 3:75-94 (1998); Eichler et al., Med. Res. Rev. 15:481-496 (1995); and the like. Libraries containing large numbers of natural and synthetic agents also can be obtained from commercial sources. Combinatorial libraries of molecules can be prepared using well known combinatorial chemistry methods (Gordon et al., J. Med. Chem. 37: 1233-1251 (1994); Gordon et al., J. Med. Chem. 37: 1385-1401 (1994); Gordon et al., Acc. Chem. Res. 29:144-154 (1996); Wilson and Czarnik, eds., Combinatorial Chemistry: Synthesis and Application, John Wiley & Sons, New York (1997)).

The invention further provides a method of diagnosing or predicting clinical prognosis of a pathology characterized by an increased or decreased level of a PAAD domain-containing polypeptide in a subject. The method includes the steps of (a) obtaining a test sample from the subject; (b) contacting the sample with an agent that can bind a PAAD domain-containing polypeptide of the invention under suitable conditions, wherein the conditions allow specific binding of the agent to the PAAD domain-containing polypeptide; and (c) comparing the amount of the specific binding in the test sample with the amount of specific binding in a reference

sample, wherein an increased or decreased amount of the specific binding in the test sample as compared to the reference sample is diagnostic of, or predictive of the clinical prognosis of, a pathology. The agent can be, 5 for example, an anti-PAAD antibody, a PAAD-associated-polypeptide (PAP), or a PAAD domain encoding nucleic acid.

Exemplary pathologies for diagnosis or the 10 prediction of clinical prognosis include any of the pathologies described herein, such as neoplastic pathologies (e.g. cancer), autoimmune diseases, and other pathologies related to abnormal cell proliferation or abnormal cell death (e.g. apoptosis), as disclosed 15 herein.

The invention also provides a method of diagnosing cancer or monitoring cancer therapy by contacting a test sample from a patient with a PAAD 20 domain specific antibody. The invention additionally provides a method of assessing prognosis (e.g., predicting the clinical prognosis) of patients with cancer comprising contacting a test sample from a patient with a PAAD domain specific antibody.

25 The invention additionally provides a method of diagnosing cancer or monitoring cancer therapy by contacting a test sample from a patient with a oligonucleotide that selectively hybridizes to a PAAD 30 domain encoding nucleic acid molecule. The invention further provides a method of assessing prognosis (e.g., predicting the clinical prognosis) of patients with cancer by contacting a test sample from a patient with a oligonucleotide that selectively hybridizes to a PAAD 35 domain encoding nucleic acid molecule.

The methods of the invention for diagnosing cancer or monitoring cancer therapy using a PAAD domain specific antibody or oligonucleotide or nucleic acid that selectively hybridizes to a PAAD domain encoding nucleic acid molecule can be used, for example, to segregate patients into a high risk group or a low risk group for diagnosing cancer or predicting risk of metastasis or risk of failure to respond to therapy. Therefore, the methods of the invention can be advantageously used to determine, for example, the risk of metastasis in a cancer patient, or the risk of an autoimmune disease of a patient, or as a prognostic indicator of survival or disease progression in a cancer patient or patient with an autoimmune disease. One of ordinary skill in the art would appreciate that the prognostic indicators of survival for cancer patients suffering from stage I cancer can be different from those for cancer patients suffering from stage IV cancer. For example, prognosis for stage I cancer patients can be oriented toward the likelihood of continued growth and/or metastasis of the cancer, whereas prognosis for stage IV cancer patients can be oriented toward the likely effectiveness of therapeutic methods for treating the cancer. Accordingly, the methods of the invention directed to measuring the level of or determining the presence of a PAAD domain-containing polypeptide or PAAD domain encoding nucleic acid can be used advantageously as a prognostic indicator for the presence or progression of a cancer or response to therapy.

30

The invention further provides methods for introducing a PAAD domain encoding nucleic acid into a cell in a subject, for example, for gene therapy. Viruses are specialized infectious agents that can elude host defense mechanisms and can infect and propagate in

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specific cell types. Viral based systems provide the advantage of being able to introduce relatively high levels of the heterologous nucleic acid into a variety of cells. Suitable viral vectors for introducing an
5 invention PAAD domain encoding nucleic acid into mammalian cells (e.g., vascular tissue segments) are well known in the art.

The present invention also provides therapeutic
10 compositions useful for practicing the therapeutic methods described herein. Therapeutic compositions of the present invention, such as pharmaceutical compositions, contain a physiologically compatible carrier together with an invention PAAD domain-containing
15 polypeptide (or functional fragment thereof), an invention PAAD domain encoding nucleic acid, an agent that alters PAAD activity or expression identified by the methods described herein, or an anti-PAAD antibody, as described herein, dissolved or dispersed therein as an
20 active ingredient. In a preferred embodiment, the therapeutic composition is not immunogenic when administered to a mammal or human patient for therapeutic purposes.

25 As used herein, the terms "pharmaceutically acceptable", "physiologically compatible" and grammatical variations thereof, as they refer to compositions, carriers, diluents and reagents, are used interchangeably and represent that the materials are capable of
30 administration to a mammal without the production of undesirable physiological effects such as nausea, dizziness, gastric upset, and the like.

The preparation of a pharmacological
35 composition that contains active ingredients dissolved or

dispersed therein is well known in the art. Typically such compositions are prepared as injectables either as liquid solutions or suspensions; however, solid forms suitable for solution, or suspension, in liquid prior to use can also be prepared. The preparation can also be emulsified.

The active ingredient can be mixed with excipients which are pharmaceutically acceptable and compatible with the active ingredient in amounts suitable for use in the therapeutic methods described herein. Suitable excipients are, for example, water, saline, dextrose, glycerol, ethanol, or the like, as well as combinations of any two or more thereof. In addition, if desired, the composition can contain minor amounts of auxiliary substances such as wetting or emulsifying agents, pH buffering agents, and the like, which enhance the effectiveness of the active ingredient.

Physiologically tolerable carriers are well known in the art. Exemplary liquid carriers are sterile aqueous solutions that contain no materials in addition to the active ingredients and water, or contain a buffer such as sodium phosphate at physiological pH, physiological saline or both, such as phosphate-buffered saline. Still further, aqueous carriers can contain more than one buffer salt, as well as salts such as sodium and potassium chlorides, dextrose, polyethylene glycol and other solutes.

As described herein, an "effective amount" is a predetermined amount calculated to achieve the desired therapeutic effect, i.e., to alter the protein binding activity of a PAAD domain-containing polypeptide or the catalytic activity of a PAAD domain-containing

polypeptide, resulting in altered biochemical process modulated by a PAAD domain-containing polypeptide. The required dosage will vary with the particular treatment and with the duration of desired treatment; however, it is anticipated that dosages between about 10 micrograms and about 1 milligram per kilogram of body weight per day will be used for therapeutic treatment. It may be particularly advantageous to administer such agents in depot or long-lasting form as discussed herein. A therapeutically effective amount is typically an amount of an agent identified herein that, when administered in a physiologically acceptable composition, is sufficient to achieve a plasma concentration of from about 0.1 µg/ml to about 100 µg/ml, preferably from about 1.0 µg/ml to about 50 µg/ml, more preferably at least about 2 µg/ml and usually 5 to 10 µg/ml. Therapeutic invention anti-PAAD antibodies can be administered in proportionately appropriate amounts in accordance with known practices in this art.

20

Also provided herein are methods of treating pathologies characterized by abnormal cell proliferation, abnormal cell death, or inflammation said method comprising administering an effective amount of an invention therapeutic composition. Such compositions are typically administered in a physiologically compatible composition.

Exemplary abnormal cell proliferation diseases associated with PAAD domain-containing polypeptides contemplated herein for treatment according to the present invention include cancer pathologies, keratinocyte hyperplasia, neoplasia, keloid, benign prostatic hypertrophy, inflammatory hyperplasia, fibrosis, smooth muscle cell proliferation in arteries

following balloon angioplasty (restenosis), and the like. Exemplary cancer pathologies contemplated herein for treatment include, gliomas, carcinomas, adenocarcinomas, sarcomas, melanomas, hamartomas, leukemias, lymphomas, and the like. Further diseases associated with PAAD domain-containing polypeptides contemplated herein for treatment according to the present invention include inflammatory diseases and diseases of cell loss. Such diseases include allergies, inflammatory diseases including arthritis, lupus, Schrogen's syndrome, Crohn's disease, ulcerative colitis, as well as allograft rejection, such as graft-versus-host disease, and the like. PAAD domain-containing polypeptides can also be useful in design of strategies for preventing diseases related to abnormal cell death in conditions such as stroke, myopyrinial infarction, heart failure, neurodegenerative diseases such as Parkinson's and Alzheimer's diseases, and for immunodeficiency associated diseases such as HIV infection, HIV-related disease, and the like.

Methods of treating pathologies can include methods of modulating the activity of one or more oncogenic proteins, wherein the oncogenic proteins specifically interact with a PAAD domain-containing polypeptide of the invention. Methods of modulating the activity of such oncogenic proteins will include contacting the oncogenic protein with a substantially pure PAAD domain-containing polypeptide or an active fragment (i.e., oncogenic protein-binding fragment) thereof. This contacting will alter the activity of the oncogenic protein, thereby providing a method of treating a pathology caused by the oncogenic protein. Further methods of modulating the activity of oncogenic proteins will include contacting the oncogenic protein with an

agent, wherein the agent alters interaction between a PAAD domain-containing polypeptide and an oncogenic protein.

5 Also contemplated herein, are therapeutic methods using invention pharmaceutical compositions for the treatment of pathological disorders in which there is too little cell division, such as, for example, bone marrow aplasias, immunodeficiencies due to a decreased
10 number of lymphocytes, and the like. Methods of treating a variety of inflammatory diseases with invention therapeutic compositions are also contemplated herein, such as treatment of sepsis, fibrosis (e.g., scarring), arthritis, graft versus host disease, and the like.

15

 The present invention also provides methods for diagnosing a pathology that is characterized by an increased or decreased level of a biochemical process to determine whether the increased or decreased level of the
20 biochemical process is due, for example, to increased or decreased expression of a PAAD domain-containing polypeptide or to expression of a variant PAAD domain-containing polypeptide. As disclosed herein, such biochemical processes include apoptosis, NFkB induction,
25 cytokine processing, caspase-mediated proteolysis, transcription, inflammation, cell adhesion, and the like. The identification of such a pathology, which can be due to altered association of a PAAD domain-containing polypeptide with a PAAD-associated polypeptide in a cell,
30 or altered ligand binding or catalytic activity of a PAAD domain-containing polypeptide, can allow for intervention therapy using an effective agent or a nucleic acid molecule or an antisense or dsRNA nucleotide sequence as described herein. In general, a test sample can be
35 obtained from a subject having a pathology characterized

by having or suspected of having increased or decreased apoptosis and can be compared to a reference sample from a normal subject to determine whether a cell in the test sample has, for example, increased or decreased

5 expression of a PAAD domain encoding gene. The level of a PAAD domain-containing polypeptide in a cell can be determined by contacting a sample with a reagent such as an anti-PAAD antibody or a PAAD-associated polypeptide, either of which can specifically bind a PAAD domain-

10 containing polypeptide. For example, the level of a PAAD domain-containing polypeptide in a cell can be determined by well known immunoassay or immunohistochemical methods using an anti-PAAD antibody (see, for example, Reed and Godzik et al., Anal. Biochem. 205:70-76 (1992); see,

15 also, Harlow and Lane, supra, (1988)). As used herein, the term "reagent" means a chemical or biological molecule that can specifically bind to a PAAD domain-containing polypeptide or to a bound PAAD/PAAD-associated polypeptide complex. For example, either an anti-PAAD

20 antibody or a PAAD-associated polypeptide can be a reagent for a PAAD domain-containing polypeptide, whereas either an anti-PAAD antibody or an anti-PAAD-associated polypeptide antibody can be a reagent for a PAAD:PAAD-associated polypeptide complex.

25

As used herein, the term "test sample" means a cell or tissue specimen that is obtained from a subject and is to be examined for expression of a PAAD domain encoding gene in a cell in the sample. A test sample can

30 be obtained, for example, during surgery or by needle biopsy and can be examined using the methods described herein to diagnose a pathology characterized by increased or decreased apoptosis. Increased or decreased expression of a PAAD domain encoding gene in a cell in a

35 test sample can be determined, for example, by comparison

to an expected normal level of PAAD domain-containing polypeptide or PAAD domain encoding mRNA in a particular cell type. A normal range of PAAD domain-containing polypeptide or PAAD domain encoding mRNA levels in various cell types can be determined by sampling a statistically significant number of normal subjects. In addition, a reference sample can be evaluated in parallel with a test sample in order to determine whether a pathology characterized by increased or decreased apoptosis is due to increased or decreased expression of a PAAD domain encoding gene. The test sample can be examined using, for example, immunohistochemical methods as described above or the sample can be further processed and examined. For example, an extract of a test sample can be prepared and examined to determine whether a PAAD domain-containing polypeptide in the sample can associate with a PAAD-associated polypeptide in the same manner as a PAAD domain-containing polypeptide from a reference cell or whether, instead, a variant PAAD domain-containing polypeptide is expressed in the cell.

In accordance with another embodiment of the present invention, there are provided diagnostic systems, preferably in kit form, comprising at least one invention PAAD domain encoding nucleic acid, PAAD domain-containing polypeptide, and/or anti-PAAD antibody described herein, in a suitable packaging material. In one embodiment, for example, the diagnostic nucleic acids are derived from any of SEQ ID NOs:15, 17, 19, 21, 23, 25 or 27. Invention diagnostic systems are useful for assaying for the presence or absence of PAAD domain encoding nucleic acid in either genomic DNA or in transcribed PAAD domain encoding nucleic acid, such as mRNA or cDNA.

A suitable diagnostic system includes at least one invention PAAD domain encoding nucleic acid, PAAD domain-containing polypeptide, and/or anti-PAAD antibody, preferably two or more invention nucleic acids, proteins
5 and/or antibodies, as a separately packaged chemical reagent(s) in an amount sufficient for at least one assay. Instructions for use of the packaged reagent are also typically included. Those of skill in the art can readily incorporate invention nucleic acid probes and/or
10 primers into kit form in combination with appropriate buffers and solutions for the practice of the invention methods as described herein.

As employed herein, the phrase "packaging
15 material" refers to one or more physical structures used to house the contents of the kit, such as invention nucleic acid probes or primers, and the like. The packaging material is constructed by well known methods, preferably to provide a sterile, contaminant-free
20 environment. The packaging material has a label which indicates that the invention nucleic acids can be used for detecting a particular PAAD domain encoding sequence including the nucleotide sequences set forth in SEQ ID
NOs:15, 17, 19, 21, 23, 25 or 27 or mutations or
25 deletions therein, thereby diagnosing the presence of, or a predisposition for a pathology such as cancer or an autoimmune disease. In addition, the packaging material contains instructions indicating how the materials within the kit are employed both to detect a particular sequence
30 and diagnose the presence of, or a predisposition for a pathology such as cancer or an autoimmune disease.

The packaging materials employed herein in relation to diagnostic systems are those customarily
35 utilized in nucleic acid-based diagnostic systems. As

used herein, the term "package" refers to a solid matrix or material such as glass, plastic, paper, foil, and the like, capable of holding within fixed limits an isolated nucleic acid, oligonucleotide, or primer of the present invention. Thus, for example, a package can be a glass vial used to contain milligram quantities of a contemplated nucleic acid, oligonucleotide or primer, or it can be a microtiter plate well to which microgram quantities of a contemplated nucleic acid probe have been operatively affixed.

"Instructions for use" typically include a tangible expression describing the reagent concentration or at least one assay method parameter, such as the relative amounts of reagent and sample to be admixed, maintenance time periods for reagent/sample admixtures, temperature, buffer conditions, and the like.

A diagnostic assay should include a simple method for detecting the amount of a PAAD domain-containing polypeptide or PAAD domain encoding nucleic acid in a sample that is bound to the reagent. Detection can be performed by labeling the reagent and detecting the presence of the label using well known methods (see, for example, Harlow and Lane, supra, 1988; chap. 9, for labeling an antibody). A reagent can be labeled with various detectable moieties including a radiolabel, an enzyme, biotin or a fluorochrome. Materials for labeling the reagent can be included in the diagnostic kit or can be purchased separately from a commercial source. Following contact of a labeled reagent with a test sample and, if desired, a control sample, specifically bound reagent can be identified by detecting the particular moiety.

A labeled antibody that can specifically bind the reagent also can be used to identify specific binding of an unlabeled reagent. For example, if the reagent is an anti-PAAD antibody, a second antibody can be used to
5 detect specific binding of the anti-PAAD antibody. A second antibody generally will be specific for the particular class of the first antibody. For example, if an anti-PAAD antibody is of the IgG class, a second antibody will be an anti-IgG antibody. Such second
10 antibodies are readily available from commercial sources. The second antibody can be labeled using a detectable moiety as described above. When a sample is labeled using a second antibody, the sample is first contacted with a first antibody, then the sample is contacted with
15 the labeled second antibody, which specifically binds to the first antibody and results in a labeled sample.

All patents, publications and database sequences mentioned herein are incorporated in their
20 entirety by reference thereto. The invention will now be described in greater detail by reference to the following non-limiting examples.

EXAMPLES

25

1.0 Identification of PAAD domain-containing polypeptides.

The sequence of the N-terminal 100 amino acid
30 fragment of the pyrin protein (Genbank Accession # NP00234; Pras, 1998, Scand. J. Rheumatol., 27:92-97) was used to perform a cascade of PSI-BLAST searches until no new hits were found. Lower significance hits from this procedure (called Saturated BLAST) were confirmed using
35 the profile-to-profile alignment algorithm FFAS

(Rychlewski et al., 2000, Protein Science 9:232-241) against a library of apoptosis-related domains. Proteins suspected of having a PAAD domain were added to the Saturated BLAST and FFAS databases and the FFAS similarity score was used to accept or reject the putative PAAD domains. Most of the proteins identified in Figures 1 and 2 could be connected with each other with PSI-BLAST significance better than 0.001 and/or the FFAS Z-score better than 10. The weakest link in the chain is the connection between the AIM2/IFI16 branch and the rest of the family (pyrin / ASC / caspase / NAC), with 0.05 PSI-BLAST E-value and FFAS Z-score of 8. The latter value was independently verified on a protein structure benchmark to give a correct match in more than 99% of cases (Rychlewski et al. supra). The same link was also confirmed by independent application of the Gibbs sampling algorithm (Lawrence, C. et al. (1993) Science 262:208-14), where sequence patterns identified in the pyrin/ASC/caspase branch of the family could be consistently used to find the AIM2/IFI16 group, albeit with low significance. In accordance with the present invention, this Saturated BLAST procedure resulted in the identification of several putative PAAD homologues in the unfinished nucleotide databases.

25

The process of gene identification and assembling include the following steps:

A) Identification of new candidate PAAD containing polypeptides. A iterative database search was performed using the TBLASTN program with the PAAD domain of pyrin and all other identified PAAD domains as the query in the following NCBI databases: high throughput genome sequence (HTGS), genomic survey sequence (GSS) and expressed sequence tag (EST) databases.

B) Verification that the new candidate PAAD domain-containing polypeptide is novel. Using PSI-BLAST, each new candidate PAAD domain gene was queried in the annotated non-redundant (NR) database at NCBI. When the new candidate gene showed significant but not identical homology with other known PAAD domain-containing polypeptides during this search, the PAAD domain-containing polypeptide candidate was kept for further analysis.

C) 3-D-Model Building of new candidate PAAD domain polypeptide: When the sequence homology was low (<25% identity), three-dimensional criteria was added to characterization of new PAAD domain-containing polypeptides. The candidate PAAD domain fragment was analyzed by a profile-profile sequence comparison method which aligns the candidate PAAD domain with a database of sequences of known three-dimensional structure. From this analysis, a sequence alignment was produced and a model three-dimensional structure was built using DD, DED and CARD domains as templates. In most cases, the best score was produced using PAAD domain sequences having known three-dimensional structures. The quality of the three-dimensional model obtained from the alignments confirmed that novel PAAD domain-containing polypeptides had been identified.

D) Identification of additional domains in the full length protein. Full length protein sequences were obtained using the new PAAD domain identified in step B as query. TBLASTN searches of the sequences containing the newly identified PAAD domains were performed. Longer aligned fragments or multiple aligned fragments in the accession number corresponding to the newly identified

PAAD domain-containing polypeptides indicated a longer PAAD domain-containing protein.

E) These additional domains were assembled using the following gene building procedure:

Genomic DNA fragments identified by T-BLAST-N analysis were extended and identified using exon prediction programs, such as Genescan, GRAIL, ORF-find, and the like; searching in both directions until start and stop codons were identified.

2.0 Identification of PAAD domain-containing polypeptides PAN2-6, Pyrin2 and ASC2.

Nucleic acids encoding PAAD domain-containing proteins corresponding to PAN2, PAN3, PAN4, PAN5, PAN6, Pyrin2 and ASC2 were identified from different PAAD domain queries using tblastn and systematically scanning gss, htgs, and all EST databases at NCBI. Further analysis using translated genomic fragments containing PAAD domains, which fragments were larger than the PAAD domain itself as query, were performed to identify additional domains. Genomic DNA were translated in all reading frames and examined for additional domains using psi-blast and nr database. Using this strategy, additional domains of PAAD domain-containing polypeptides, including a NB-ARC domain, LRR repeat and ANGIO-R domain, were identified.

3.0 Cloning and sequencing of large cDNA.

For cDNA larger than 1500 bp, cloning is accomplished by amplification of multiple fragments of the cDNA. Jurkat total RNA is reverse-transcribed to

complementary DNAs using MMLV reverse transcriptase (Stratagene) and random hexanucleotide primers.

Overlapping cDNA fragments of a PAAD domain-containing polypeptide are amplified from the Jurkat complementary
5 DNAs with Turbo *Pfu* DNA polymerase (Stratagene) using an oligonucleotide primer set for every 1500 bp of cDNA, where the amplified cDNA fragment contains a unique restriction site near the end that is to be ligated with an adjacent amplified cDNA fragment.

10

The resultant cDNA fragments are ligated into mammalian expression vector pcDNA-myc (Invitrogen, modified as described in Roy et al., EMBO J. 16:6914-6925 (1997)) and assembled to full-length cDNA by

15 consecutively ligating adjacent fragments at the unique endonuclease sites form the full-length cDNA. Sequencing analysis of the assembled full-length cDNA is carried out, and splice isoforms of PAAD domain-containing polypeptides can be identified.

20

4.0 *Plasmid Constructions.*

Complementary DNA encoding a PAAD domain-containing polypeptide, or a functional fragment thereof
25 is amplified from Jurkat cDNAs with Turbo *Pfu* DNA polymerase (Stratagene) and desired primers, such as those described above. The resultant PCR fragments are digested with restriction enzymes such as *EcoRI* and *Xho I* and ligated into pGEX-4T1 (Pharmacia) and pcDNA-myc
30 vectors.

5.0 *In vitro Protein Binding Assays.*

PAAD domain-containing or fragments thereof
35 encoded in pGEX-4T1 are expressed in XL-1 blue *E. coli*

cells (Stratagene), and affinity-purified using glutathione (GSH)-sepharose according to known methods, such as those in Current Protocols in Molecular Biology, Ausubel et al. eds., John Wiley and Sons (1999). For GST pull-down assays, purified PAAD domain GST fusion proteins and GST alone (0.1-0.5 µg immobilized on 10-15 µl GSH-sepharose beads) are incubated with 1 mg/ml of BSA in 100 µl Co-IP buffer [142.4 mM KCl, 5mM MgCl₂, 10 mM HEPES (pH 7.4), 0.5 mM EGTA, 0.2% NP-40, 1 mM DTT, and 1 mM PMSF] for 30 min. at room temperature. The beads are then incubated with 1 µl of rat reticulocyte lysates (TnT-lysate; Promega, Inc.) containing ³⁵S-labeled, *in vitro* translated PAAD domain-containing or control protein Skp-1 in 100 µl Co-IP buffer supplemented with 0.5 mg/ml BSA for overnight at 4°C. The beads are washed four times in 500 µl Co-IP buffer, followed by boiling in 20 µl Laemmli-SDS sample buffer. The eluted proteins are analyzed by SDS-PAGE. The bands of SDS-PAGE gels are detected by fluorography.

20

The resultant oligomerization pattern will reveal that PAAD:PAAD and other protein:protein interactions occur with invention PAAD domain-containing polypeptides (e.g., PAN2 through PAN6, and the like) or fragments thereof.

In vitro translated candidate PAAD-associated polypeptides, along with a control, are subjected to GST pull-down assay using GSH-sepharose beads conjugated with GST and GST-PAAD domain-containing polypeptides as described above. Lanes containing GST-PAAD domain yield positive binding signals when incubated with a PAAD-associated polypeptide selected from Apaf-1, CED4, Nod1/CARD4, ASC-1, CARDX1, pro-Casp1, pro-Casp2, pro-Casp4, pro-Casp5, pro-Casp7, pro-Casp11, pro-Casp12, pro-

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Casp14, CED3, Dronc, Raidd/CRADD, Cardiak (RIP2, Rick), Bcl-1/CIPER, ARC, NOP30, cIAP-1, cIAP-2, Fadd/mort1, pro-Casp8, pro-Casp10, Dredd, c-Flip/flame, KSV/V-Flip, MCV, DEDD/DEFT, PEA-15, Flash, BAP31, BAR, RIP, IRAK-1, IRAK-2, IRAK-M, My D88, NMP-84, Ankyrin-1, Ankyrin-3, TNFR1, NGFR, Fas, DR3, DR4, DR5, DR6, Tradd, Fadd, Raidd2, DAP Kinase, NIK, IKK α , IKK β , I κ B, p65, p50, IKAP, pyrin, pyrin2, PAN1, PAN2, PAN3, PAN4, PAN5, PAN6, ASC, ASC2, NAC, AIM2, IFI16, MO13L, p52, p100, p105, ParaCaspase (MALT1), and all members of the NF κ B/I κ B families, whereas, the controls GST alone and Skp-1 yield negligible signals.

6.0 *Self-Association of NB-ARC domain of PAAD domain-containing polypeptides.*

In vitro translated, ³⁵S-labeled rabbit reticulocyte lysates (1 μ l) containing an NB-ARC domain of an invention PAN protein or a control protein, such as SKP-1, are incubated with GSH-sepharose beads conjugated with purified GST-NB-ARC or GST alone for GST pull-down assay, resolved on SDS-PAGE and visualized by fluorography as described above. One tenth of input is loaded for NB-ARC or Skp-1 as controls. The results indicate that the NB-ARC domains of invention PAN proteins can self-associate by binding through the NB-ARC domains.

7.0 *Protein-Protein Interactions of PAAD domain-containing polypeptides.*

Transient transfections of 293T, a human embryonic kidney fibroblast cell line, are conducted using SuperFect reagents (Qiagen) according to manufacturer's instructions. 293T cells are transiently

transfected with an expression plasmid (2 µg) encoding HA-tagged Apaf-1, CED4, Nod1/CARD4, ASC-1, CARDX1, pro-Casp1, pro-Casp2, pro-Casp4, pro-Casp5, pro-Casp7, pro-Casp11, pro-Casp12, pro-Casp14, CED3, Dronc, Raidd/CRADD, 5 Cardiak (RIP2, Rick), Bcl-1/CIPER, ARC, NOP30, cIAP-1, cIAP-2, Fadd/mort1, pro-Casp8, pro-Casp10, Dredd, c-Flip/flame, KSV/V-Flip, MCV, DEDD/DEFT, PEA-15, Flash, BAP31, BAR, RIP, IRAK-1, IRAK-2, IRAK-M, My D88, NMP-84, Ankyrin-1, Ankyrin-3, TNFR1, NGFR, Fas, DR3, DR4, DR5, 10 DR6, Tradd, Fadd, Raidd2, DAP Kinase, NIK, IKKα, IKKβ, IκB, p65, p50, IKAP, pyrin, pyrin2, PAN1, PAN2, PAN3, PAN4, PAN5, PAN6, ASC, ASC2, NAC, AIM2, IFI16, MO13L, p52, p100, p105, ParaCaspase (MALT1), and all members of the NFκB/IκB families, or the like, in the presence or 15 absence of a plasmid (2 µg) encoding a myc-tagged PAAD domain-containing polypeptide. After 24 hr growth in culture, transfected cells are collected and lysed in Co-IP buffer [142.4 mM KCl, 5 mM MgCl₂, 10 mM HEPES (pH 7.4), 0.5 mM EGTA, 0.1 % NP-40, and 1 mM DTT] supplemented with 20 12.5 mM β-glycerolphosphate, 2 mM NaF, 1 mM Na₃VO₄, 1 mM PMSF, and 1X protease inhibitor mix (Boehringer Mannheim). Cell lysates are clarified by microcentrifugation and subjected to immunoprecipitation using either a mouse monoclonal antibody to myc (Santa 25 Cruz Biotechnologies, Inc) or a control mouse IgG. Proteins from the immune complexes are resolved by SDS-PAGE, transferred to nitrocellulose membranes, and subjected to immunoblot analysis using anti-HA antibodies followed by anti-myc antibodies using a standard Western 30 blotting procedure and ECL reagents from Amersham-Pharmacia Biotechnologies, Inc. (Krajewski et al., Proc. Natl. Acad. Sci. USA 96:5752-5757 (1999)).

The results indicate that invention PAAD 35 domain-containing polypeptides can bind to themselves

(e.g., homodimers, and the like) and to one or more polypeptides selected from Apaf-1, CED4, Nod1/CARD4, ASC-1, CARDX1, pro-Casp1, pro-Casp2, pro-Casp4, pro-Casp5, pro-Casp7, pro-Casp11, pro-Casp12, pro-Casp14, CED3, Dronc, Raidd/CRADD, Cardiak (RIP2, Rick), Bcl-1/CIPER, ARC, NOP30, cIAP-1, cIAP-2, Fadd/mort1, pro-Casp8, pro-Casp10, Dredd, c-Flip/flame, KSV/V-Flip, MCV, DEDD/DEFT, PEA-15, Flash, BAP31, BAR, RIP, IRAK-1, IRAK-2, IRAK-M, My D88, NMP-84, Ankyrin-1, Ankyrin-3, TNFR1, NGFR, Fas, DR3, DR4, DR5, DR6, Tradd, Fadd, Raidd2, DAP Kinase, NIK, IKK α , IKK β , I κ B, p65, p50, IKAP, pyrin, pyrin2, PAN1, PAN2, PAN3, PAN4, PAN5, PAN6, ASC, ASC2, NAC, AIM2, IFI16, MO13L, p52, p100, p105, ParaCaspase (MALT1), and all members of the NF κ B/I κ B families.

15

8.0 Cloning and Characterization of PAN2

As a first step in cloning PAN2 cDNA, RT-PCR was performed on total RNA from HeLa cells using oligo dT to prime the first-strand synthesis and then 2 PAN2-specific primers designated Pan2/5':

5'-CCGGAATTCACCATGGCAGCCTCTTCTTCTCTGATTTT-3' (SEQ ID NO:35) and Pan2/3':

5'-CCGCTCGAGTCACGTAGAGCTGTGTTTCATCCTCTTTCTTAA-3' (SEQ ID NO:36). These primers were designed based on the predicted PAN2 open reading frame identified in the genomic sequence AC022066, as described in Example 2.0. The ATG of PAN2 and an artificial stop codon inserted after amino acid 620 are underlined in SEQ ID NOS:35 and 36, respectively. EcoRI and XhoI restriction sites are shown in italics in SEQ ID NOS:35 and 36, respectively. The resulting PCR product was cloned into a pcDNA3Myc expression vector at the EcoRI(5') and XhoI(3'), and sequenced.

35

A BLAST search of the human EST database was then performed using the partial PAN2 sequence. Several EST clones were identified, and several corresponding I.M.A.G.E. Consortium cDNA clones (Lennon et al.,
5 Genomics 33;151-152 (1996)) were obtained. I.M.A.G.E. Consortium CloneID 3139498, corresponding to EST GenBank Accession Number BE278926, was sequenced and determined to contain full-length PAN2 cDNA, including the stop codon, the 3' UTR of the gene and the poly-A tail.

10

The complete coding sequence of PAN2 was cloned by PCR from I.M.A.G.E. Consortium CloneID 3139498 by PCR, using as the 5' primer SEQ ID NO:35 and as the 3' primer Pan2STOP4: 5'-CCTCTCGAGTCAGATCTCTACCCTTGTGATTGTGTCAC-3'
15 (SEQ ID NO:40). The PAN2 cDNA was independently amplified from HeLa cells using overlapping primers to confirm that the I.M.A.G.E. clone contained an intact, single cDNA. The PAN2 cDNA coding sequence (SEQ ID NO:15) is 2985 nucleotides and encodes an amino acid
20 sequence (SEQ ID NO:16) of 995 amino acids.

Several domains within PAN2 were identified, based on homology with known proteins. The PAAD domain (SEQ ID NO:2) corresponds to amino acids 14-89 of SEQ ID
25 NO:16. The nucleotide-binding domain (NB-ARC) (SEQ ID NO:37) corresponds to amino acids 147-336 of SEQ ID NO:16. The Angiotensin receptor-like domain (AR-like) (SEQ ID NO:38) corresponds to amino acids 465-605 of SEQ ID NO:16. The Leucine rich region (LRR) (SEQ ID NO:39)
30 corresponds to amino acids 620-995 of SEQ ID NO:16.

Expression of PAN2 in human tissues was determined using a panel of Clontech (Palo Alto, CA) first-strand cDNAs to amplify a region of PAN2
35 corresponding to the NB-ARC domain (amino acids 147-465),

following manufacturer's recommended procedures. PAN2 was found to be expressed in several human tissues, including placenta, lung, liver, muscle, kidney, pancreas, spleen, thymus, prostate, testis and ovary.

5

In order to determine whether the PAAD domain of PAN2 is able to self-associate, fusions of the PAN2 PAAD domain (amino acids 1-89 of SEQ ID NO:16) and PAN2(1-620) (amino acids 1-620 of SEQ ID NO:16) with glutathione-S-transferase (GST) were constructed, expressed in bacteria and attached to glutathione beads. The GST fusion proteins were used to pull down *in vitro*-translated PAN2 PAAD or PAN2(1-620). GST alone and GST-CD40 were used as controls. The PAAD domain of PAN2 was determined not to self-associate or to associate with PAN2. However, PAN2(1-620) was determined to self-associate, likely through its NB-ARC domain. Therefore, the PAAD domain is likely not involved in PAN2/PAN2 interactions.

20

The effect of expression of the PAN2 PAAD domain on NF- κ B activation by the TNF α pathway and the IL-1 β pathway were assessed as follows. 10,000 293N cells were seeded into 96-well plates and cells were transfected the following day using SuperFect™ transfection reagent (Qiagen, Venlo, The Netherlands) with 10 ng of pNF κ B-luc and 2.5 ng of thymidine kinase promoter-Renilla luciferase (pRL-TK) reporter vectors (Stratagene, San Diego, CA), together with 100 ng of plasmids encoding proteins in the TNF- α pathway (pCMV TNFR1, pcDNA3 Traf2 or pcDNA3HA RIP) or in the IL-1 β pathway (pCMVFlag IL-1R, pcDNA3His MyD88, pcDNA3HA IRAK3 or pcDNA3HA Traf6), and either 400 ng of pcDNA3Myc ("Empty") or 400 ng of pcDNA3Myc PAAD 1-89 ("PAAD"). After 36 hours, cells were harvested and luciferase

activities were determined using the Dual Luciferase System (Promega, Madison, Wisconsin).

The results of the luciferase assays for cells transfected with molecules in the TNF α pathway are shown in Table 1, below. For the "TNF α " condition, cells were stimulated with 10 ng TNF α for 6-8 hours prior to lysis. The numbers indicate the fold induction of NF κ B activity.

Table 1:

	TNFR1	TNF α	TRAF2	RIP
EMPTY	20.04	21.05	33.53	53.93
PAAD2	19.62	7.14	15.75	23.51

The results of the luciferase assays for cells transfected with molecules in the IL-1 β pathway are shown in Table 2, below. The numbers indicate the fold induction of NF κ B activity.

Table 2:

	IL1R	MyD88	IRAK2	TRAF6
EMPTY	6	28.16	10.27	28.17
PAAD2	4.27	21.23	4.58	20.41

The results of the NF κ B activation assays shown in Tables 1 and 2 indicate that expression of the PAAD domain of PAN2 significantly inhibits NF κ B activation by either the TNF α or the IL-1 β pathway.

Expression of full-length PAN2 was also demonstrated to inhibit NF κ B activation by either the TNF α or the IL-1 β pathway. At the same DNA concentration, the inhibition of NF κ B activation

following transfection with pcDNA3Myc PAN2 was almost the same as the extent of inhibition following transfection with pcDNA3Myc PAAD 1-89. It was concluded that inhibition of NF κ B activation by PAN2 was mediated by the PAAD domain.

In order to determine whether PAN2 affects activation of NF κ B mediated by upstream components in the NF κ B activation pathway, plasmids encoding either NIK (pCMV-NIK), IKK α (pRE-HA-IKK α) or IKK β (pRE-HA-IKK β) were co-transfected into 293N cells as described above with from 10ng to 300ng of pcDNA3Myc PAN2 or with empty vector, together with 10 ng of pNF κ B-luc and 2.5 ng of pTK-RL. Luciferase activities determined as described above. As shown in Figure 5, PAN2 expression dose-dependently blocked the activation of NF κ B mediated by either NIK, IKK α or IKK β . Therefore, PAN2 acts downstream of the I κ B kinase complex.

NF κ B is normally sequestered into the cytoplasm of nonstimulated cells by a family of inhibitory proteins, called I κ B (α , β , γ and ϵ). Exposure of cells to various stimuli leads to the rapid phosphorylation, ubiquitination and proteolytic degradation of I κ B, which frees NF κ B to translocate to the nucleus where it regulates gene expression. Accordingly, it was hypothesized that the PAN2 inhibitory effect on NF κ B activation could be related to I κ B. To test this hypothesis, the *in vivo* interactions between PAN2 and I κ B α were determined.

For co-immunoprecipitation experiments, HEK293T cells were seeded at 3×10^6 cells per well in 100mm dishes and transfected with 6-8 μ g plasmid DNA using Lipofectamine Plus[™] transfection reagent (GIBCO) 24 hours

later. After culturing for 36 hours, cells were collected, washed in PBS and lysed in isotonic lysis buffer [150 or 500 mM NaCl, 20 mM Tris/HCl (pH 7.4), 1% NP-40, 12.5 mM β -glycerophosphate, 2 mM NaF, 1 mM Na_3VO_4 , 1 mM PMSF, and 1X protease inhibitor mix (Roche)]. Lysates were clarified by centrifugation and subjected to immunoprecipitation using agarose-conjugated anti-c-Myc antibodies (Santa Cruz) or anti-FlagM2 antibodies (Sigma) or non-specific control antibodies and Protein G-agarose for 2-4 hours at 4°C. Immune-complexes were washed 3-5 times with lysis buffer and once with PBS, boiled in 1.5X Laemmli buffer, and separated by 12-15% PAGE. Immune-complexes were then transferred to PVDF membranes (Millipore) and immunoblotted with anti-c-Myc (Santa Cruz) or anti-Flag (Sigma) antibodies in 5% dry milk in TBS-T. Membranes were washed, incubated with HRP-conjugated secondary antibodies, and reactive proteins were detected using ECL.

As shown in Figure 6, Flag-tagged I κ B α co-immunoprecipitated with Myc-tagged PAN2 ("f.l.") when both plasmids were expressed in 293T cells.

In order to determine which domain of PAN2 is responsible for association with I κ B, the following constructs were co-expressed in 293T cells with Flag-tagged I κ B α or an empty Flag-tagged vector: Myc-tagged full-length PAN2, Myc-tagged PAN2 Δ LRR (amino acids 1-619 of PAN2), Myc-tagged PAN2PAAD (amino acids 1-89 of PAN2), Myc-tagged PAN2NBARC (amino acids 147-465 of PAN2), or Myc-tagged PAN2AR-like (amino acids 336-605 of PAN2). Immunoprecipitation and immunoblot assays were performed as described above.

As shown in Figure 6, Flag-tagged I κ B α co-immunoprecipitated with Myc-tagged full-length PAN2 ("f.l."), Myc-tagged PAN2 Δ LRR, and Myc-tagged PAN2NBARC, each of which contained the NBARC domain, but not with
5 Myc-tagged PAN2PAAD or Myc-tagged PAN2AR-like.

These results indicate that the NBARC domain of PAN2 is responsible for association with I κ B α , whereas the PAAD domain of PAN2 is responsible for inhibition of
10 NF κ B interaction.

9.0 Cloning and Characterization of PAN5

In order to clone PAN5 cDNA, first strand cDNA
15 was synthesized at 42°C for 1 hour from HeLa total RNA (1 μ g) using the PAN5 specific primer (300 ng): L1515 (reverse): TTGCTCGAGTCATCTGAATAC (SEQ ID NO:53), and the ProStart Ultra HF RT-PCR system (Stratagene) as described by the manufacturer. A control mRNA and primers provided
20 in the kit were also used (positive control). The completed first-strand cDNA was used for PCR amplification using Pfu DNA polymerase (2.5 units) and PAN5-specific primers (100ng each), U1 (forward): ATGGCCATGGCCAAGGC CAGAAAGC (SEQ ID NO:54) and L1515
25 (reverse): TTGCTCGAGTCATCTGAATAC (SEQ ID NO:55). The following PCR conditions were used: 4' hot start at 94°C, 35 cycles of 94°C denaturation for 1 minute, 44°C annealing for 1 minute and extension at 72°C for 2 minutes and a final 10 minute extension at 72°C. A 1515 bp PCR
30 product corresponding to PAN5 was observed on an agarose gel. The resultant PCR product was cloned into pcDNA4-His/Max Topo (Invitrogen) following the recommendations of the manufacturer.

The PAAD domain of PAN5 ("PAAD5"), corresponding to bp34-271 of PAN5 cDNA (SEQ ID NO:21), encoding amino acids 12-90 of SEQ ID NO:22, was amplified by PCR from a HeLa cDNA library using the primer set
5 EA-PAC5-Eco-U34: GAATTCCTCTGGGCCTTGAGTGACCTTGAG (SEQ ID NO:51) and EA-PAC5-Xho-St-L271: CCAGCCGACCTCGAGCAGTCAAATATGGC (SEQ ID NO:52). PCR reactions contained in a total volume of 50 µl: 10x PCR buffer, 20 mM each dNTPs, amplitaq polymerase (0.5 U),
10 100 ng HeLa cDNA, 50ng of each primer and 10% DMSO. The same mixture lacking DNA was used as a negative control. The PCR conditions used were as follows: the DNA was first denatured for 3 minutes (hot start). The primer mixture was then added and for 30 subsequent cycles of
15 PCR, the samples were denatured at 94°C for 30 seconds, annealed at 44°C for 30 seconds and extended at 72°C for 1 minute. The 30 cycles of PCR were followed by a 10 minute extension at 72°C.

20 The PAAD5 domain was first cloned into pCR-II-Topo, sequence-verified and then digested with EcoR1/Xho1. The digest was then analyzed by gel electrophoresis and the 238 bp band containing the PAAD5 domain gel purified for subcloning into pCDNA3-Myc at the
25 EcoR1/XhoI sites for expression in mammalian cells.

In order to determine the effect of PAN5 or the PAAD5 domain on NFκB activation, HEK293 cells were transiently transfected using SuperFect™ transfection
30 reagent (1.5 µl/well) with pNFκB-Luc (50 ng) and pRL-TK (10 ng) luciferase reporter constructs, pCDNA3-PAAD5 or pCDNA4-PAN5 (390 ng) and 50 ng each of different components of the TNF, LPS or IL signaling pathways, as indicated in Table 3. After incubation for 3 hours, the
35 transfection reagent was removed, fresh serum-containing

media was added and cells were then incubated for 36 hours. After 36 hours, cells were lysed with Passive lysis buffer (1x; Promega) and then the effect of PAAD5 domain or PAN5 on NF κ B activity was measured with a
 5 luminometer. Co-transfection of pToF-Flash/ β -catenin was used as a control for stickiness.

The results of the luciferase assays are shown in Table 3, below.

10

Table 3:

<u>Construct</u>	<u>NFκB Activity (fold induction)</u>
Control	1
TNF α	24
15 PAAD5	3
PAN5	4
TNFR1	23
TNFR1/PAAD5	21
TNFR1/PAN5	24
20 NIK	30
NIK/PAAD5	5
NIK/PAN5	3
IKK β	45
IKK β /PAAD5	6
25 IKK β /PAN5	8
p65	55
p65/PAAD5	13
p65/PAN5	46
ToF-Flash+ β -catenin	16
30 ToF-Flash+ β -catenin/PAAD5	15
ToF-Flash+ β -catenin/PAN5	17

As evidenced by the data shown in Table 3, overexpression of either PAN5, or the PAAD domain of PAN5, inhibits NF κ B activation by a variety of proteins in the TNF, LPS or IL signaling pathways. Therefore, the
5 PAAD domain of PAN5, like the PAAD domain of other PAN proteins described herein, is responsible for the inhibition of NF κ B activation.

In order to determine the expression of PAN5 in
10 human tissues, a commercially available Northern membrane (Stratagene) was prehybridized with QuikHyb hybridization solution (Stratagene) containing single stranded sperm DNA for 1-2 hours at 68°C. ³²P- primer labeling of the DNA probe (the 1.5 kb fragment corresponding to the PAN5
15 ORF) was performed at 37°C for 30 minutes, using the RTS radprime DNA labeling kit (Life Technologies), as described by the manufacturer. The ³²P- primer labeling reaction contained 25 ng of denatured DNA, dATP, dAGTP, dTTP, random octamer primers, 50 μ Ci [³²P] dCTP and Klenow
20 fragment. The prehybridization solution was removed, and the denatured radiolabeled probe was added to the hybridization solution (same as prehybridization buffer) and the membrane was hybridized overnight at 68°C. The membrane was washed three times for 40' with 2x SSC/0.05%
25 SDS at room temperature, washed twice for 40' at 50°C, and exposed to Kodak XAR-5 film with intensifying screens at -70°C C for 1-3 days.

Two transcripts, of 1.8 kb and 1.35 kb, were
30 found to be expressed at varying levels in most human tissues tested. Thymus, spleen, placental and lung had the highest expression of PAD5 transcripts. In thymus and spleen, the 1.35 kb transcript was more abundant than the 1.8 kb transcript, whereas in placenta the 1.8 kb

transcript was more abundant than the 1.35 kb transcript.

10.0 Cloning and Characterization of PAN6

5 The PAAD domain of PAN6 ("PAAD6") corresponding to bp34-271 of PAN6 cDNA (SEQ ID NO:23), encoding amino acids 12-90 of SEQ ID NO:24, was amplified by PCR from HeLa cDNA library using the primer set EA-PAAD6-U22: GACGGATCCTGTGGCATGGCCACCTACTTGG (SEQ ID NO:56) and
10 EA-PAAD6-L291: ATCCCTCACGAATCCCCTCACTGTCCTC (SEQ ID NO:57), essentially as described for PAAD5. The PAAD 6 domain was first cloned into pCR-II- Topo, sequence-verified and then digested with BamH1 and Xho1. The 270 bp band containing the PAAD 6 domain was gel purified and,
15 ligated into pcDNA3-Myc for expression in mammalian cells, into pGEX-4T.3 for GST-fusion protein production and into pGilda for yeast two-hybrid studies, at the BamH1/Xho1 sites of the relevant vector.

20 In order to determine the effect of PAAD6 expression on NFkB activation, HEK293 cells were transiently transfected with pNFkB-Luc (50 ng) and pRL-TK (10 ng) luciferase reporter constructs, pcDNA3-PAAD6(390 ng) and 50 ng each of different components of the TNF,
25 LPS or IL signaling pathways, as indicated in Table 4, as described above for PAAD5.

 The results of the luciferase assays are shown in Table 4, below.

Table 4:

	<u>Construct</u>	<u>NFκB Activity (fold induction)</u>
	Control	1
5	TNFα	20
	PAAD6	4
	IRAK2	18
	IRAK2/PAAD6	2
	TRAF2	44
10	TRAF2/PAAD6	5
	TRAF6	45
	TRAF6/PAAD6	6
	NIK	29
	NIK/PAAD6	3
15	RIP	45
	RIP/PAAD6	2
	p65	50
	p65/PAAD6	11
	IKKβ	42
20	IKKβ/PAAD6	2
	Bcl10	10
	Bcl10/PAAD6	1
	Nod1	17
	Nod1/PAAD6	18
25	TNFR1	25
	TNFR1/PAAD6	19
	ToF-Flash+β-catenin	18
	ToF-Flash+β-catenin/PAAD6	17

30 As evidenced by the data shown in Table 4,
overexpression of the PAAD domain of PAN6 inhibits NFκB

activation by a variety of proteins in the TNF, LPS or IL
signaling pathways. Therefore, the PAAD domain of PAN6,
like the PAAD domain of other PAN proteins described
herein, is responsible for the inhibition of NF κ B
5 activation.

In order to identify proteins that associate
with PAN6 in vivo, the pGilda plasmid was used to express
as a "bait" protein the PAAD domain of PAN6 (nucleotides
10 22-291 of PAN6 cDNA, corresponding to amino acids 8-97 of
SEQ ID NO:24). The plasmid expressing the LexA-PAAD6
bait protein was then used to transform the yeast strain
EGY48 (MAT, trp1, ura3, his, his leu2::6LexAop-LEU2. The
ability of the LexA-PAAD6 bait protein alone to activate
15 LEU2 or LacZ reporter genes was also tested. The
LexA-PAAD6 bait protein was used to screen a human
fetal brain and Jurkat T cell pJG4-5 cDNA libraries.
Briefly, cells were grown in either YPD medium with 1%
yeast extract, 2% polypeptone and 2% glucose, or in
20 Burkholder's minimal medium (BMM) supplemented with
appropriate amino acids. Transformations were performed
by a LiCl method using 0.1 mg of pJG4-5 cDNA library DNA
and 5 mg denatured salmon sperm DNA. The potential
positive transformants that grew on Leu deficient BMM
25 plates containing 2% galactose were transferred to BMM
plates containing leucine and 2% glucose. Filter assays
were then performed to measure β -galactosidase activity
as described in Sato et al. Proc. Natl. Acad. Sci USA
91:9238-9242 (1994). As a result of the screening, 7
30 β -galactosidase positive clones out of 11 clones from the
Jurkat T cell cDNA library were obtained that
transactivated the LEU2 reporter gene (based on the
ability to grow on leu deficient media). The screening
of a fetal brain cDNA library gave 430 positive clones
35 for the transactivation of the LEU2 reporter gene. Of

those, 42 colonies were also positive in the β -galactosidase assay.

Two of the clones identified as encoding
5 PAAD6-interacting proteins by yeast two hybrid analysis
encoded IKAP, which is an IK β kinase complex associated
protein. The region of IKAP that interacted with PAAD6
was within amino acids 1089-1232. IKAP is known in the
art and described, for example, in Cohen et al., Nature
10 395:292-296 (1998).

In order to determine the expression of PAN6 in
human tissues, a commercially available Northern membrane
(Stratagene) was hybridized as described above in regard
15 to PAN5 expression, using the EST I.M.A.G.E. clone
2900568, corresponding to nucleotides 892-2331 of PAN6 as
the radiolabeled probe.

A PAN6 transcript of 3.3 kb was observed at
20 highest levels in thymus, spleen and skeletal muscle,
with lower levels in other tissues.

11.0 Cloning and characterization of ASC and ASC2

25 ASC and ASC2 were cloned as following. The ASC
or ASC2 (SEQ ID NO:27) open reading frames, or the ASC
CARD or PAAD domains, were amplified by high fidelity PCR
using primers containing EcoRI and XhoI sites and sub
cloned into pcDNA3 vectors containing Myc, Flag or HA
30 epitope tags on the N-or C-terminal end. As template
either the ASC cDNA described in Masumoto et al., J.
Biol. Chem. 274:33835-33838 (1999) or the 619 bp EST with
GenBank Accession No. W73523 (gi:1383656) were used.
Authenticity of all constructs was confirmed by DNA
35 sequencing. The primers used were as follows:

ASC: 5'-GAATTCGATCCTGGAGCCATGGGG-3' (SEQ ID NO:41);

5'-CTCGAGCCGGAGTGTGCTGGGAA-3' (SEQ ID NO:42);

ASC-PAAD: 5'-GAATTCGATCCTGGAGCCATGGGG-3 (SEQ ID NO:43);

5 5'-CTCGAGTCAGCTTGGCTGCCGACT-3' (SEQ ID NO:44) or

5-CCCCCTCGAGGGCCTGGCTTGGCTGCCGACT-3' (SEQ ID NO:45);

ASC-CARD: 5'- GAATTCCTCAGTCGGCAGCCAAG-3' (SEQ ID NO:46);

5'-CTCGAGCCGGAGTGTGCTGGGAA-3' (SEQ ID NO:47);

10

ASC2: 5'- GAATTCGAGGCGCAGGGCTGTG-3' (SEQ ID NO:48);

5'-CTCGAGGCTTACAGGCGTTGCAT-3' (SEQ ID NO:49) or

5'-CTCGAGGCTACAGGCGTTGCAT-3' (SEQ ID NO:50).

15

ASC contains a PAAD domain at the N-terminus followed by a CARD domain. ASC2 contains only a PAAD domain, which shares extensive sequence homology with the PAAD domain of ASC. The ASC gene is localized at chromosome 16p12-11.2, whereas the ASC2 gene is localized at chromosome 16.p13.

To determine associations between various domains of ASC and ASC2, GST pull-down assays and yeast two-hybrid assays were performed. For GST pull-down assays, ASC-PAAD and ASC2 were subcloned into pGEX4-T1 (Pharmacia) and affinity purified as GST-fusion proteins from *E.coli* XL-1 blue (Stratagene) using GSH-Sepharose. Purified GST-fusion proteins (0.1 µg) immobilized on 10-15 µl of GSH-Sepharose beads were incubated with 1 mg/ml bovine serum albumin in 100µl buffer A [142.4 mM KCl, 5 mM MgCl₂, 10 mM HEPES (pH 7.4), 0.5 mM EGTA, 1 mM EDTA, and 0.2% Nonidet P-40, supplemented with 1 mM dithiothreitol, 12.5 mM β-glycerol phosphate, 1 µM Na₃VO₄, 1 mM phenylmethylsulfonyl fluoride, and 1X protease inhibitor mix (Roche)] for 30 min at 25°C. The beads were

washed twice and incubated overnight at 4°C with 1 µl of rabbit reticulocyte lysate (Quick-TNT-lysate, Promega) containing ³⁵S-labeled, *in vitro*-translated proteins in 100 µl of buffer A supplemented with 0.5 mg/ml bovine
5 serum albumin. Bound proteins were washed four times in 500 µl of buffer A, followed by boiling in 20 µl of Laemmli-SDS sample buffer, SDS-PAGE and detected by fluorography.

10 By the GST pull-down assays, the PAAD domain of ASC did not associate with the CARD domain of ASC, but weakly associated with full-length ASC and with ASC2, suggesting that the PAAD domain of ASC self-associates and also associates with ASC2.

15 For the yeast two-hybrid assays, the yeast EGY-48 strain was transformed with various combinations of ASC, ASC-CARD, ASC-PAAD, and ASC2 in the plasmids pGilda and pJG 4-5, together with the β-galactosidase
20 expression plasmid pSH-18-34 (Invitrogen). Colonies were plated on both LEU+ and LEU- media and also used for a β-Gal-assay. The results of the yeast interaction assays are shown in Table 5, below.

Table 5:

	pJG 4-5	pGilda	Leu	β -Gal
	ASC-CARD	ASC-CARD	+	+
5	ASC-CARD	empty	-	-
	ASC-CARD	ASC	+	+
	ASC-CARD	ASC-PAAD	-	-
	ASC-CARD	ASC2	-	-
	ASC-PAAD	empty	-	-
10	ASC-PAAD	ASC-PAAD	+	+
	ASC2	empty	-	-
	ASC2	ASC2	+	-
	ASC2	ASC	+	+
15	ASC	empty	-	-

As shown in Table 5, the CARD domain of ASC self associates. In this *in vivo* assay, the PAAD domain of ASC was shown to self-associate, and also to associate with ASC2.

20

For co-immunoprecipitation experiments, HEK293T cells were seeded at 5×10^5 cells per well in six-well plates (35mm wells) and transfected with 2 μ g plasmid DNA using Superfect (Qiagen) 24 hours later. After

25 culturing for 36 hours, cells were collected, washed in PBS and lysed in isotonic lysis buffer [150 or 500 mM NaCl, 20 mM Tris/HCl (pH 7.4), 0.2% NP-40, 12.5 mM β -glycerophosphate, 2 mM NaF, 1 mM Na_3VO_4 , 1 mM PMSF, and 1X protease inhibitor mix (Roche). Lysates were

30 clarified by centrifugation and subjected to immunoprecipitation using agarose-conjugated anti-c-Myc antibodies (Santa Cruz), anti-HA antibodies (Santa Cruz, Roche) anti-FlagM2 antibodies (Sigma) or non-specific control antibodies and Protein G-agarose for 2-4 hours at

4°C. Immune-complexes were washed 3-5 times with lysis buffer and once with PBS, boiled in 1.5X Laemmli buffer, and separated by 12-15% PAGE next to 10% of the total lysate. Immune-complexes were then transferred to PVDF membranes (Millipore) and immunoblotted with anti-c-Myc (Santa Cruz), anti-HA (Roche), or anti-Flag (Sigma) antibodies in 5% dry milk in TBS-T. Membranes were washed, incubated with HRP-conjugated secondary antibodies, and reactive proteins were detected using ECL.

The results of the co-immunoprecipitation assays are shown in Table 6, below, with a "+" sign indicating co-immunoprecipitation.

Table 6:

	Myc-ASC	HA-ASC	+
	Myc-Caspase-1	HA-ASC	+
20	Myc-Card10	HA-ASC	+
	Flag-Nod1	HA-ASC	+
	Flag-Cardiak	HA-ASC	+
	Myc-ASC2	HA-ASC-PAAD	+
	Flag-Nod1	HA-ASC-PAAD	+
25	Flag-Cardiak	HA-ASC-PAAD	+
	Myc-NIK	HA-ASC-PAAD	+
	Flag-IKK-i	HA-ASC-PAAD	+
	Flag-I κ B α	HA-ASC-PAAD	-
30	HA-IKK β	Myc-ASC-PAAD	-

The results shown in Table 6 indicate that ASC associates with ASC, ASC2, Caspase-1, Card10, Nod1, Cardiak, NIK and IKK-i.

GST pull-down assays, as described above, were used to determine whether the CARD domain of ASC is able to associate with other proteins, including other CARD domain-containing proteins. The results of these assays are shown in Table 7, with a "+" indicating a detectable interaction between the GST-ASC-CARD domain and the indicated *in vitro*-translated (IVT) test protein.

Table 7:

10

	GST-ASC-CARD/IVT Caspase-8	-
	GST-ASC-CARD/IVT Caspase-9	-
	GST-ASC-CARD/IVT Caspase-10	-
	GST-ASC-CARD/IVT Bcl-10	-
15	GST-ASC-CARD/IVT RAIDD	-
	GST-ASC-CARD/IVT ASC-2	-
	GST-ASC-CARD/IVT ASC	+
	GST-ASC-CARD/IVT Xiap	-
	GST-ASC-CARD/IVT cIAP-1	-
20	GST-ASC-CARD/IVT cIAP-2	-

As shown in Table 7, the CARD domain of ASC, while self-associating, does not associate with several other CARD domain-containing proteins.

25

In order to determine the localization of ASC and ASC2, Cos-7 cells were seeded onto 12-well plates and transfected with 1.5 µg total fusion plasmid DNA (either EGFP-ASC, EGFP-ASC2 or EGFP-ASC in combination with RFP-ASC2) (Clontech) using Lipofectamine plus (Life Technologies) 24 hours later. The next day cells were trypsinized and seeded onto 4- or 8-well chamber slides (LabTec) and fixed with 4% paraformaldehyde and mounted

30

(Vectashield). Confocal laser scanning microscopy was then performed.

The microscopy results indicated that ASC, when
5 expressed alone, was localized to characteristic
"speckles." ASC2, when expressed alone, exhibited a
diffuse pattern of cytoplasmic and nuclear localization.
However, when expressed together, ASC and ASC2 co-
localized in ASC speckles. Therefore, ASC is apparently
10 able to recruit ASC2 into ASC "speckles." This co-
localization is further evidence that ASC and ASC2
associate *in vivo*.

In order to determine the effect of ASC, ASC-
15 CARD, ASC-PAAD and ASC2 on NF κ B induction in response to
TNF α , IL-1 β , Bcl10, Nod1 or Cardiak, reporter assays were
performed using the Dual-Luciferase assay system
(Promega). In brief, HEK293N cells were seeded onto
24-well plates and transfected with 1 μ g total plasmid
20 DNA including 6 ng of pRL-TK and 150ng pRL-NF- κ B or pRL-
p53 (all Promega) using SuperFect[™] transfection reagent
(Qiagen) 24 hours later. After culturing for 48 hours,
cells were lysed in 100 μ l passive lysis buffer (Promega)
and frozen at -80°C. Subsequently, 5-10 μ l of lysate were
25 transferred to 96-well plates and analyzed using a
Luminometer (Wallach, Perkin Elmer). If indicated, cells
were treated with 10 ng TNF- α or IL-1 β 6-8 hours prior to
lysis. All experiments were performed in triplicate and
repeated at least twice.

30

As shown in Figure 7A-7C, ASC, ASC2 and the
PAAD domain of ASC are each able to inhibit NF κ B
induction by Bcl-10, TNF α and IL-1 β . As shown in Figure
7D, ASC and ASC2 also inhibited NF κ B induction by Nod1
35 and, to a lesser extent, by Cardiak. In other

experiments, the inhibition of TNF α -induced NF κ B activation was shown to be dependent on the amount of either ASC or ASC2 transfected, and also to be specific for NF κ B, as no inhibition of adriamycin-induced p53
5 activation by ASC was observed.

Certain genes are induced by NF κ B, including TRAF1 (Carpentier et al., FEBS Lett. 460:246-250 (1999). TNF α is a potent inducer of NF κ B activation. In order to
10 examine the effect of ASC-PAAD and ASC2 on TNF α -induced expression of the endogenous NF κ B target gene TRAF1, HEK 293N cells were transiently transfected with expression plasmids for ASC-PAAD or ASC2, and either treated for 4 hours with TNF α or left untreated. Cleared lysates were
15 immunoblotted with anti-TRAF1 or anti-TRAF2 antibodies. Equal loading was confirmed by re-blotting with an anti-Tubulin antibody. As shown in Figure 8, treatment with TNF normally causes an increase in expression of TRAF1 but not TRAF2 protein (see lanes marked CNTR, compare -
20 and + TNF). Expression of either ASC-PAAD or ASC2 decreased both basal and TNF-induced expression of TRAF1, without affecting expression of TRAF2. Because increased TRAF1 expression in response to TNF stimulation is mediated by NF κ B activation, this result is consistent
25 with the determination (see Figure 7) that ASC-PAAD or ASC2 inhibit NF κ B activation.

Active caspase-1 cleaves pro-IL-1 β , resulting in the generation of bioactive IL-1 β which is secreted
30 from cells. In order to determine whether ASC or ASC2 affected caspase-1-induced pro-IL-1 β processing, COS-7 cells and HEK293N cells were grown in 24 well plates (14 mm wells) and transfected with 1 μ g plasmid DNA (Myc-tagged pro-caspase-1, pro-IL-1 β (Lee et al., J.
35 Biol. Chem. 276:34495-34500 (2001); Damiano et al.,

Genomics 75:77-83 (2001)), HA-tagged ASC and HA-tagged ASC2 in various combinations) using Lipofectamine plus (Gibco BRL, Grand Island, NY) or Superfect (Qiagen, Valencia, CA) 24 hours later. After culturing for 36
5 hours at 37°C and 5% CO₂ in Dulbecco's modified Eagle medium (DMEM) supplemented with either 20% or 10% heat-inactivated fetal bovine serum (FBS), 1 mM L-glutamine, and antibiotics, supernatants were collected, volume adjusted and stored at -80°C or used
10 immediately for an IL-1 β ELISA assay (R&D Systems, Minneapolis, MN) according to the manufacturer's instructions. Cells were washed in PBS, lysed in isotonic lysis buffer, and directly analyzed by immunoblotting using anti-Myc and anti-HA antibodies.
15 Results from one representative experiment of at least three experiments are shown in Figure 9.

As shown in Figure 9, co-expression of procaspase-1 and pro-IL-1 β ("IL-1") resulted in a high
20 level of secretion of active IL-1 β . This IL-1 β secretion was inhibited by about 50% by co-expression of ASC, and almost completely inhibited by co-expression of both ASC and ASC2, but was not inhibited by expression of ASC2 alone. Therefore, ASC interferes with activation of a
25 CARD-containing caspase, caspase-1. The association between Cardiak and ASC (see Table 6) may be involved in the inhibition of caspase-1 activation.

Caspases that cleave the tetrapeptide substrate
30 DEVD-AFC are directly involved in apoptosis, and thus DEDVase activity serves as a surrogate marker of apoptosis. In order to determine the effect of ASC and ASC2 on caspase activation, HEK293N cells were transiently transfected with expression plasmids for ASC;
35 or ASC in combination with ASC2 alone or further in

combination with active site mutants of caspase-1, caspase-8, caspase-9 or caspase-10. Transfected HEK293N cells were directly lysed in caspase lysis buffer (10 mM HEPES (pH 7.4), 25 mM NaCl, 0.25% Triton X-100, and 1 mM EDTA), normalized for protein content, and protease activity was measured continuously by monitoring the release of fluorogenic Ac-DEVD-AFC (Bachem, Philadelphia, PA) at 37°C. As shown in Figure 10, caspase activity was increased by expression of ASC (A and B), and further increased by expression of ASC and ASC2 in combination (A and B). Caspase activity was only slightly increased by expression of ASC2 alone (B). Expression of catalytic site mutants of caspase-1, caspase-8 or caspase-10 (c/a) only slightly decreased ASC+ASC2-mediated caspase activity (B), whereas expression of a catalytic site mutant of caspase-9 (c/a) strongly inhibited ASC+ASC2-mediated caspase activity (B). Therefore, ASC and ASC2 activate a caspase-9-dependent pathway for apoptosis.

Although the invention has been described with reference to the examples above, it should be understood that various modifications can be made without departing from the spirit of the invention. Accordingly, the invention is limited only by the following claims.

We claim:

1. An isolated nucleic acid molecule encoding a PAAD-containing polypeptide, comprising:
 - 5 (a) a nucleic acid molecule encoding a polypeptide comprising the amino acid sequence set forth as SEQ ID NOs: 16, 18, 20, 22, 24, 26 or 28; or
 - 10 (b) a nucleic acid molecule that hybridizes to the nucleic acid molecule of (a) under highly stringent conditions, where the nucleic acid molecule encodes a biologically active PAAD domain-containing polypeptide.
- 15 2. The nucleic acid molecule of claim 1, comprising a nucleotide sequence set forth as any of SEQ ID NO: 15, 17, 19, 21, 23, 25 and 27.
3. A vector containing the nucleic acid
20 molecule of claim 1.
4. A recombinant cell containing the nucleic acid molecule of claim 1.
- 25 5. An isolated nucleic acid molecule encoding a PAAD domain, comprising:
 - 30 (a) a nucleic acid molecule encoding a PAAD domain amino acid sequence set forth as any of SEQ ID NOS: 2, 3, 4, 5, 6, 8, or 10; or
 - (b) a nucleic acid molecule that hybridizes to the nucleic acid molecule of (a) under highly stringent conditions, where the nucleic acid molecule encodes a biologically active PAAD domain.

7. A vector containing the nucleic acid molecule of claim 6.

8. A recombinant cell containing the nucleic acid molecule of claim 6.

9. An isolated nucleic acid molecule encoding an NB-ARC domain, comprising:

- 10 (a) a nucleic acid molecule encoding the NB-ARC domain amino acid set forth as any of SEQ ID NOS:37, 60, 62 or 63;
- (b) a nucleic acid molecule that hybridizes to the nucleic acid molecule of (a) under highly stringent conditions, where the nucleic acid molecule encodes a biologically active NB-ARC domain.
- 15

10. A vector containing the nucleic acid molecule of claim 9.

20

11. A recombinant cell containing the nucleic acid molecule of claim 9.

12. An isolated nucleic acid molecule encoding an LRR domain, comprising:

25

- (a) a nucleic acid molecule encoding the LRR domain amino acid set forth as any of SEQ ID NOS:39, 61 or 64; or
- (b) a nucleic acid molecule that hybridizes to the nucleic acid molecule of (a) under highly stringent conditions, where the nucleic acid molecule encodes a biologically active LRR domain.
- 30

13. A vector containing the nucleic acid molecule of claim 12.

14. A recombinant cell containing the nucleic acid molecule of claim 12.

15. An oligonucleotide comprising at least 17 nucleotides capable of specifically hybridizing with the nucleotide sequence set forth in any of SEQ ID NOS:15, 17, 19, 21, 23, 25 and 27 or the complement thereof.

16. An oligonucleotide comprising at least 50 nucleotides capable of specifically hybridizing with the nucleotide sequence set forth in any of SEQ ID NOS:15, 17, 19, 21, 23, 25 and 27 or the complement thereof.

17. An isolated PAAD domain-containing polypeptide, comprising an amino acid sequence at least 80% identical to the amino acid sequence set forth in any of SEQ ID NOS:16, 18, 20, 22, 24, 26 or 28, wherein said polypeptide is a biologically active PAAD domain-containing polypeptide.

18. The PAAD domain-containing polypeptide of claim 17, wherein said polypeptide comprises the amino acid sequence set forth as any of SEQ ID NOS:16, 18, 20, 22, 24, 26 or 28.

19. An isolated PAAD domain polypeptide, comprising an amino acid sequence at least 80% identical to the amino acid sequence set forth as any of SEQ ID NOS: 2, 3, 4, 5, 6, 8, or 10, wherein said polypeptide is a biologically active PAAD domain polypeptide.

20. An isolated PAAD domain polypeptide, comprising the amino acid sequence set forth as any of SEQ ID NOS: 2, 3, 4, 5, 6, 8, or 10.

5 21. An isolated NB-ARC domain polypeptide, comprising an amino acid sequence at least 80% identical to the amino acid sequence set forth as any of SEQ ID NOS:37, 60, 62 or 63, wherein said polypeptide is a biologically active NB-ARC domain polypeptide.

10

22. An isolated NB-ARC domain polypeptide, comprising an amino acid sequence set forth as any of SEQ ID NOS:37, 60, 62 or 63.

15 23. An isolated LRR domain polypeptide, comprising an amino acid sequence at least 80% identical to the amino acid sequence set forth as any of SEQ ID NOS:39, 61 or 64, wherein said polypeptide is a biologically active LRR domain polypeptide.

20

24. An isolated LRR domain polypeptide, comprising an amino acid sequence set forth as any of SEQ ID NOS:39, 61 or 64.

25 25. An isolated peptide comprising at least 10 contiguous amino acids of any of SEQ ID NOS:16, 18, 20, 22, 24, 26 or 28.

26. A method of producing a PAAD domain-
30 containing polypeptide comprising expressing the nucleic acid molecule of claim 1 *in vitro* or in a cell under conditions suitable for expression of said polypeptide.

27. An isolated anti-PAAD antibody having specific reactivity with the PAAD domain-containing polypeptide of claim 18.

5 28. The antibody of claim 27, wherein said antibody is a monoclonal antibody.

29. A cell line producing the monoclonal antibody of claim 29.

10

30. The antibody of claim 27, wherein said antibody is a polyclonal antibody.

31. A method of identifying a nucleic acid
15 molecule encoding a PAAD-containing polypeptide in a sample, said method comprising:

 contacting a sample containing nucleic acids with an oligonucleotide according to claim 15, wherein said contacting is effected under high stringency
20 hybridization conditions, and identifying a nucleic acid molecule which hybridizes thereto.

32. A method of detecting the presence of a PAAD domain-containing polypeptide in a sample, said
25 method comprising contacting a test sample with an antibody according to claim 27, detecting the presence of an antibody:polypeptide complex, and thereby detecting the presence of a PAAD domain-containing polypeptide in said test sample.

30

33. A method of identifying a PAAD domain-containing polypeptide-associated polypeptide (PAP) comprising the steps of:

- (a) contacting the PAAD domain-containing polypeptide of claim 17 with a candidate PAP;
- (b) detecting association of said PAAD domain-containing polypeptide with said candidate PAP, wherein a candidate PAP that associates with said polypeptide is identified as a PAP.

10

34. A method of identifying a PAP comprising the steps of:

- (a) contacting the PAAD domain polypeptide of claim 19 with a candidate PAP;
- (b) detecting association of said PAAD domain polypeptide with said candidate PAP, wherein a candidate PAP that associates with said polypeptide is identified as a PAP.

20

35. A method of identifying a PAP comprising the steps of:

- (a) contacting the NB-ARC domain polypeptide of claim 21 with a candidate PAP;
- (b) detecting association of said NB-ARC polypeptide with said candidate PAP, wherein a candidate PAP that associates with said polypeptide is identified as a PAP.

36. A method of identifying a PAP comprising the steps of:

- (a) contacting the LRR domain polypeptide of claim 23 with a candidate PAP;
- (b) detecting association of said LRR polypeptide with said candidate PAP,

wherein a candidate PAP that associates with said polypeptide is identified as a PAP.

37. A method of identifying an effective agent
5 that alters the association of a PAAD domain-containing polypeptide with a PAAD domain-containing polypeptide-associated polypeptide (PAP), comprising the steps of:

- 10 (a) contacting the PAAD domain-containing polypeptide of claim 17, or a PAAD, NB-ARC or LRR domain therefrom, and said PAP under conditions that allow said PAAD domain-containing polypeptide or said fragment and said PAP to associate, with a candidate agent; and
- 15 (b) detecting the altered association of said PAAD domain-containing polypeptide or domain with said PAP,

wherein an agent that alters said association is identified as an effective agent.

20

38. The method of claim 37, wherein said PAP is selected from the group consisting of ASC, ASC2, Caspase-1, Card10, Nod1, NIK, IKK-i, I κ B α and IKAP.

25 39. A method of identifying an agent that associates with a PAAD domain-containing polypeptide, comprising the steps of:

- (a) contacting the PAAD domain-containing polypeptide of claim 17 with a candidate agent; and
- 30 (b) detecting association of said PAAD domain-containing polypeptide with said agent.

40. A method of identifying an agent that associates with a PAAD domain polypeptide, comprising the steps of:

- (a) contacting the PAAD domain polypeptide of
5 claim 19 with a candidate agent; and
- (b) detecting association of said PAAD domain polypeptide with said agent.

41. A method of identifying an agent that
10 associates with a NB-ARC domain polypeptide, comprising the steps of:

- (a) contacting the NB-ARC domain polypeptide of claim 21 with a candidate agent; and
- (b) detecting association of said NB-ARC
15 domain polypeptide with said agent.

42. A method of identifying an agent that associates with a LRR domain polypeptide, comprising the steps of:

- 20 (a) contacting the LRR domain polypeptide of claim 23 with a candidate agent; and
- (b) detecting association of said LRR domain polypeptide with said agent.

25 43. A method of identifying an agent that modulates PAAD domain-mediated inhibition of NFkB activity, comprising the steps of:

- (a) contacting a cell that recombinantly expresses a PAAD domain-containing polypeptide with a
30 candidate agent; and
- (b) detecting NFkB activity in said cell, whereas increased or decreased NFkB activity in said cell compared to a control cell indicates that said candidate agent is an agent that modulates PAAD domain-mediated
35 inhibition of NFkB activity.

44. The method of claim 43, wherein said PAAD domain polypeptide comprises an amino acid sequence set forth as any of SEQ ID NOS:1-14.

5 45. The method of claim 43, wherein said PAAD domain polypeptide comprises an amino acid sequence at least 80% identical to the amino acid sequence set forth as any of SEQ ID NOS: 2, 3, 4, 5, 6, 8, or 10, wherein said polypeptide is a biologically active PAAD domain
10 polypeptide.

 46. The method of claim 43, wherein said cell is contacted with or recombinantly expresses an inducer of NFκB activity.
15

 47. A method of identifying an agent that modulates an activity of a NB-ARC domain of a PAAD domain-containing polypeptide, comprising the steps of:
20 (a) contacting the NB-ARC domain polypeptide of claim 21 with a candidate agent; and
 (b) detecting an activity of said NB-ARC domain, whereby an increase or decrease of said activity identifies said agent as an agent that modulates the activity of the NB-ARC domain of
25 said PAAD domain-containing polypeptide;
wherein the detected activity of said NB-ARC domain is selected from homo-oligomerization, hetero-oligomerization, nucleotide hydrolysis, and nucleotide binding.

30

48. A method of modulating NFκB transcriptional activity in a cell, comprising the steps of:

- 5 (a) introducing the nucleic acid molecule of claim 5 into a cell; and
- (b) expressing said nucleic acid molecule in said cell, whereby the expression of said nucleic acid modulates NFκB transcriptional activity in said cell.

10

49. A method of decreasing expression of a PAAD domain-containing polypeptide in a cell, comprising introducing an antisense or dsRNA nucleic molecule into a cell, wherein said antisense or dsRNA nucleic molecule

15 binds to any of SEQ ID NOS:15, 17, 19, 21, 23, 25 and 27.

1/10

[illegible]

FIGURE 1

2/10

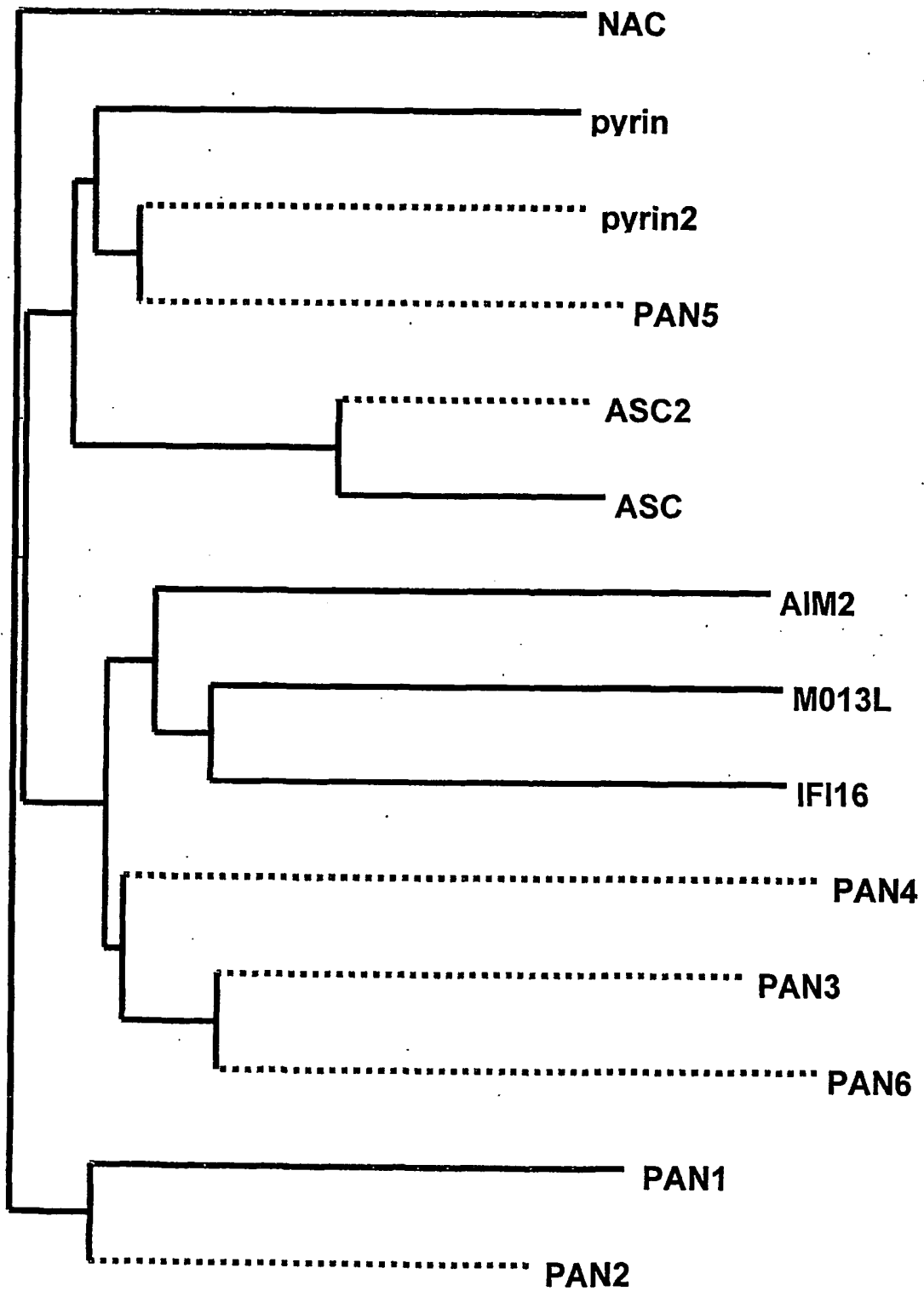


FIGURE 2 .

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ASC



PAN1 - PAN6 (only some contain leucine rich repeats - LRR)



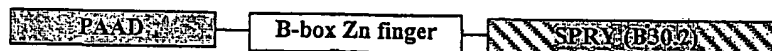
NAC



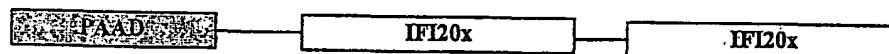
zebrafish caspase



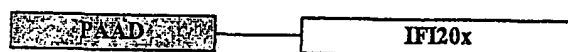
pyrin



IFI16,



AIM2, MND A



ASC2



FIGURE 3



FIGURE 4

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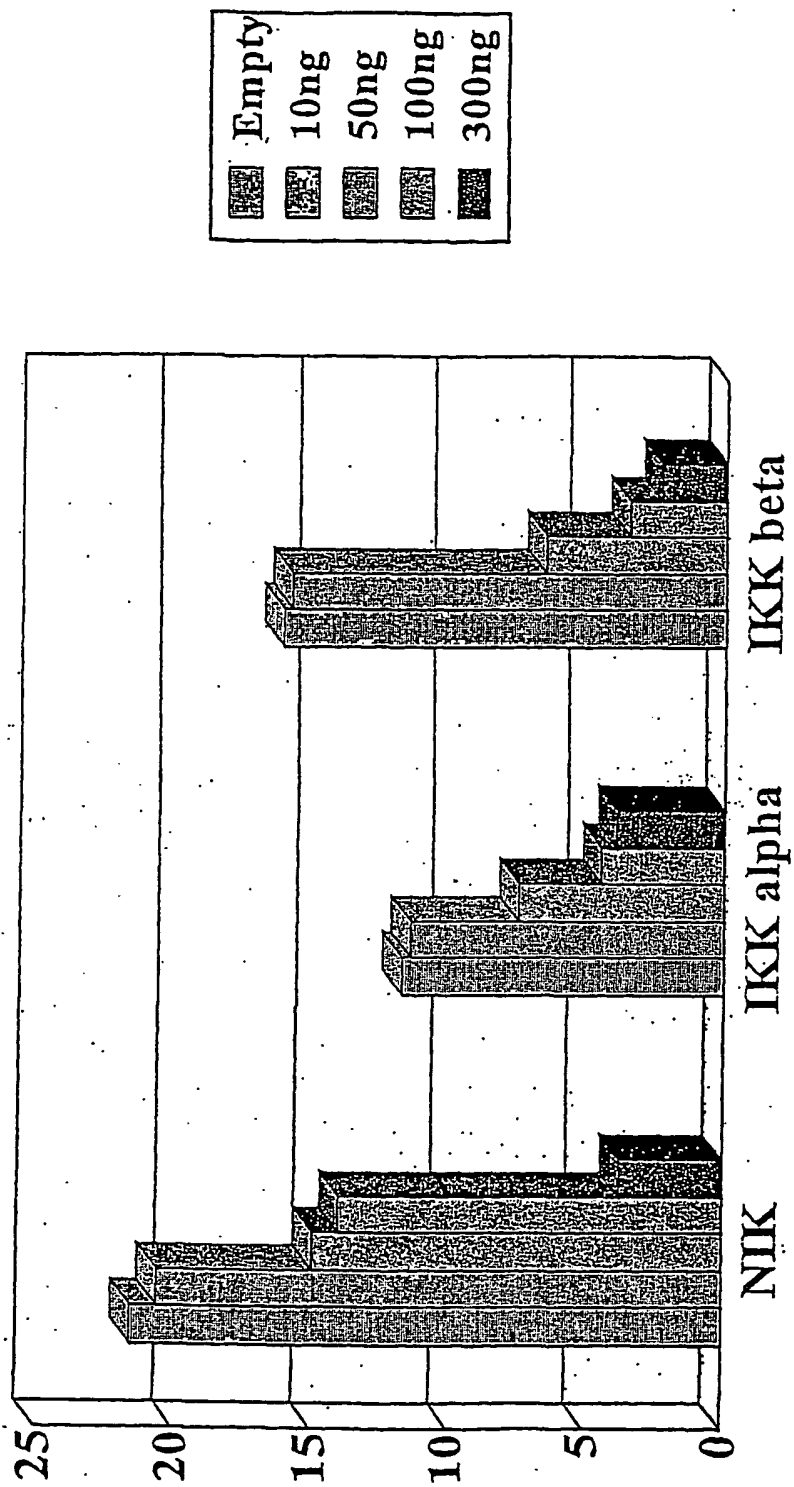


Figure 5

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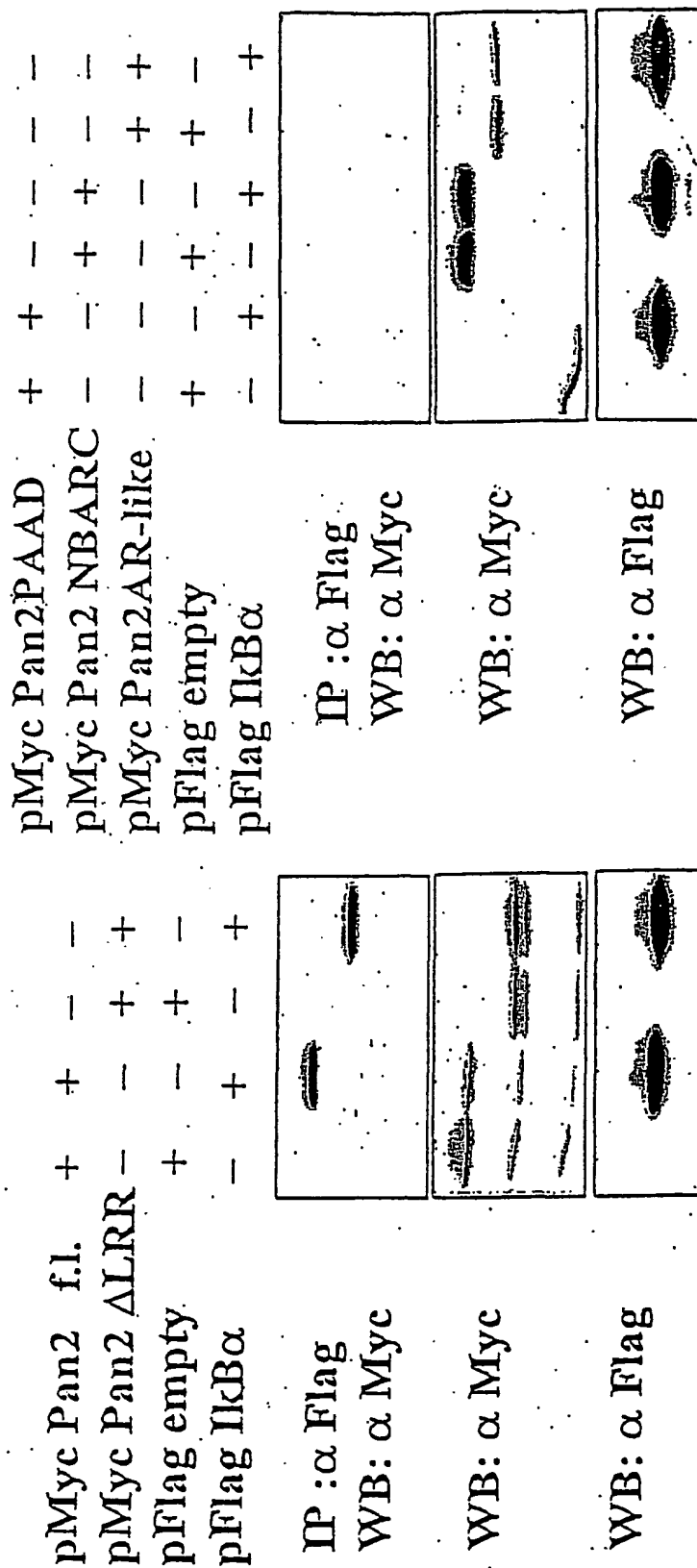


FIGURE 6

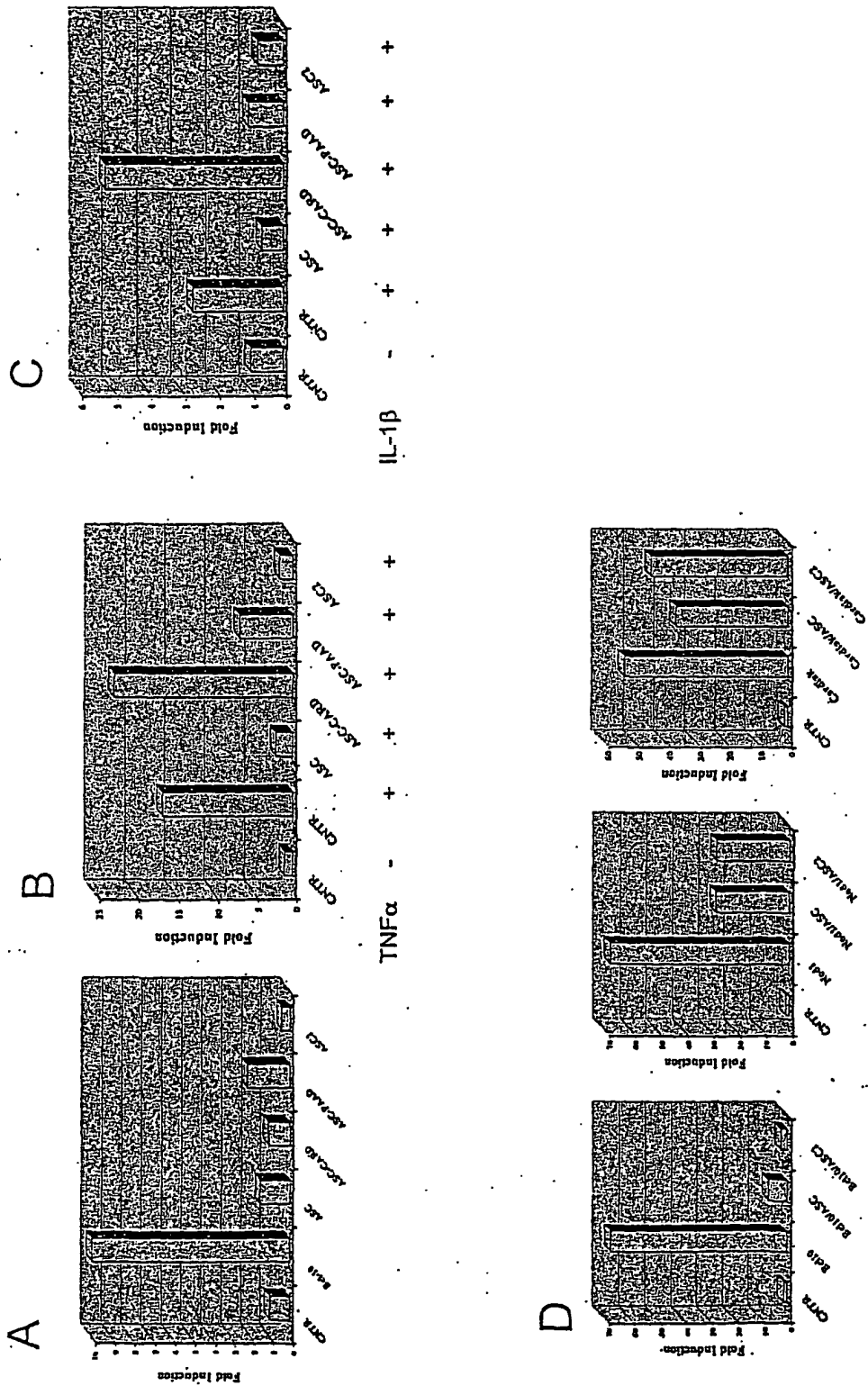


Figure 7

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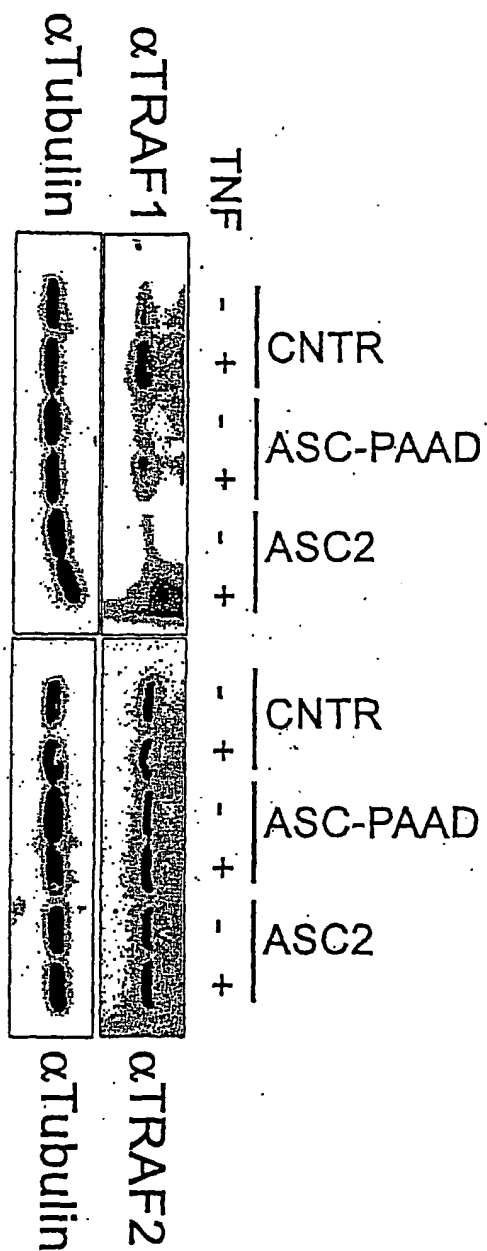


Figure 8

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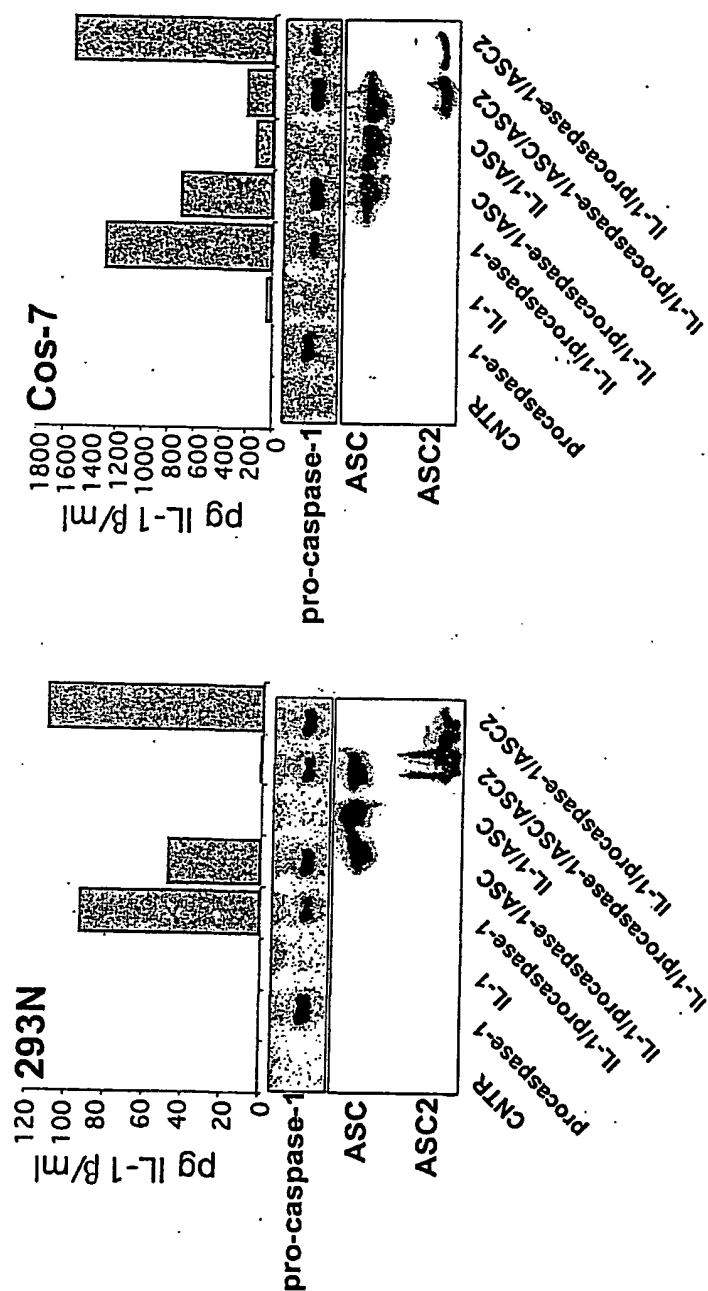


FIGURE 9

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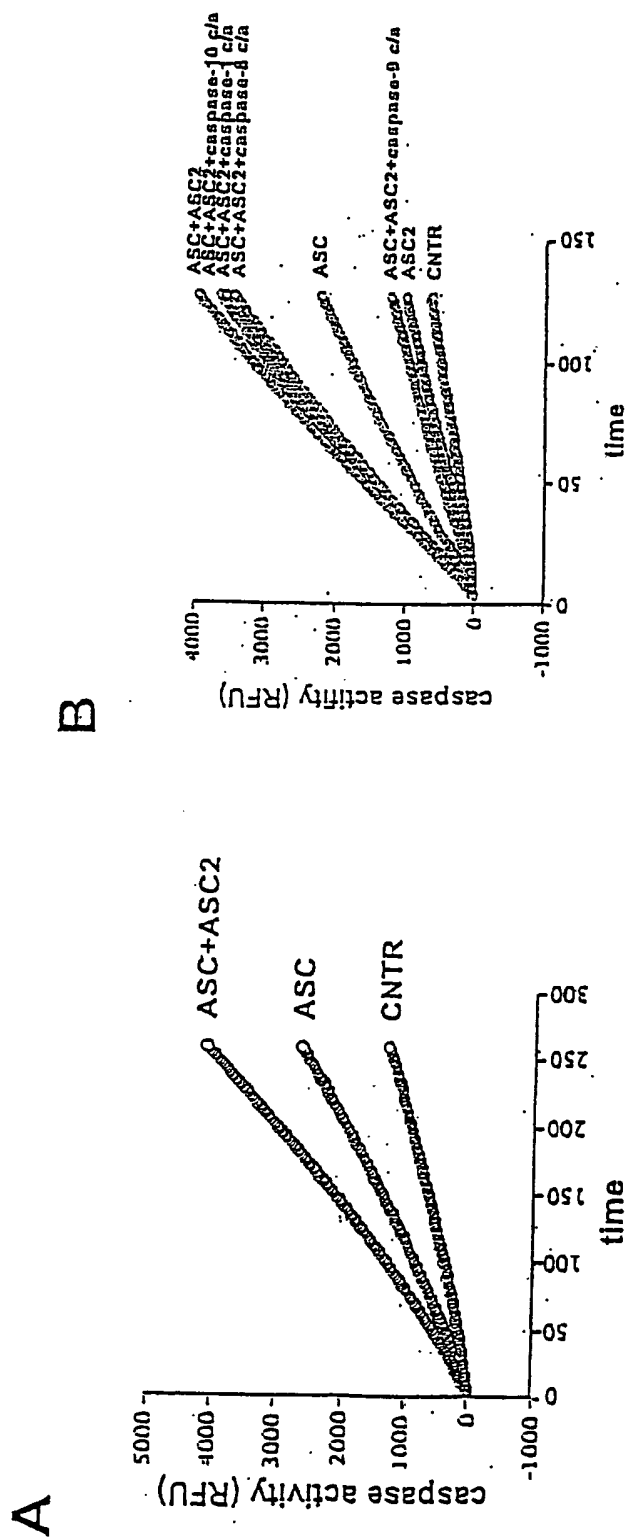


FIGURE 10



SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.

Published:

- with international search report
- with sequence listing part of description published separately in electronic form and available upon request from the International Bureau

(84) **Designated States (regional):** ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

(88) **Date of publication of the international search report:**
22 May 2003

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INTERNATIONAL SEARCH REPORT

International Application No
PCT/US 01/30160

A. CLASSIFICATION OF SUBJECT MATTER

IPC 7 C12N15/12 C12N15/11 C12N5/10 C07K14/47 C07K16/18
C12Q1/68 G01N33/50 G01N33/53

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 C07K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the International search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	<p>ARAVIND L ET AL: "The domains of death: evolution of the apoptosis machinery" TIBS TRENDS IN BIOCHEMICAL SCIENCES, ELSEVIER PUBLICATION, CAMBRIDGE, EN, vol. 24, no. 2, 1 February 1999 (1999-02-01), pages 47-53, XP004167901 ISSN: 0968-0004 figure 1</p> <p style="text-align: center;">--- -/-</p>	1

☒ Further documents are listed in the continuation of box C.

☒ Patent family members are listed in annex.

* Special categories of cited documents :

A document defining the general state of the art which is not considered to be of particular relevance

E earlier document but published on or after the international filing date

L document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

O document referring to an oral disclosure, use, exhibition or other means

P document published prior to the international filing date but later than the priority date claimed

T later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

X document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

Y document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

G document member of the same patent family

Date of the actual completion of the international search

6 September 2002

Date of mailing of the international search report

16.01.03

Name and mailing address of the ISA

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Fax (+31-70) 340-3016

Authorized officer

Nichogiannopoulou, A

INTERNATIONAL SEARCH REPORT

International Application No
PCT/US 01/30160

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	<p>KOONIN E V ET AL: "The NACHT family - a new group of predicted NTPases implicated in apoptosis and MHC transcription activation" TIBS TRENDS IN BIOCHEMICAL SCIENCES, ELSEVIER PUBLICATION, CAMBRIDGE, EN, vol. 25, no. 5, May 2000 (2000-05), pages 223-224, XP004198165 ISSN: 0968-0004 cited in the application the whole document</p>	1
A	<p>MASUMOTO J ET AL: "ASC, a novel 22-kDa protein, aggregates during apoptosis of human promyelocytic leukemia HL-60 cells" JOURNAL OF BIOLOGICAL CHEMISTRY, AMERICAN SOCIETY OF BIOLOGICAL CHEMISTS, BALTIMORE, MD, US, vol. 274, no. 48, 26 November 1999 (1999-11-26), pages 33835-33838, XP002191744 ISSN: 0021-9258 cited in the application figures 3A,3D</p>	1
A	<p>INOHARA N ET AL: "Genes with homology to mammalian apoptosis regulators identified in zebrafish." CELL DEATH AND DIFFERENTIATION, vol. 7, no. 5, May 2000 (2000-05), pages 509-510, XP002212414 ISSN: 1350-9047 cited in the application table 1</p>	1
P,X	<p>PAWLOWSKI K ET AL: "PAAD - a new protein domain associated with apoptosis, cancer and autoimmune diseases." TRENDS IN BIOCHEMICAL SCIENCES. ENGLAND FEB 2001, vol. 26, no. 2, February 2001 (2001-02), pages 85-87, XP002212415 ISSN: 0968-0004 the whole document</p>	1-4, 15-18, 25,26, 31-33
P,A	<p>FAIRBROTHER W J ET AL: "THE PYRIN DOMAIN: A MEMBER OF THE DEATH DOMAIN-FOLD SUPERFAMILY" PROTEIN SCIENCE, CAMBRIDGE UNIVERSITY PRESS, CAMBRIDGE, GB, vol. 9, no. 10, September 2001 (2001-09), pages 1911-1918, XP008006069 ISSN: 0961-8368 the whole document</p>	1

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INTERNATIONAL SEARCH REPORT

National Application No

PCT/US 01/30160

C(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT		
Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
P,A	STAUB E ET AL: "The DAPIN family: a novel domain links apoptotic and interferon response proteins." TRENDS IN BIOCHEMICAL SCIENCES. ENGLAND FEB 2001, vol. 26, no. 2, February 2001 (2001-02), pages 83-85, XP002212416 ISSN: 0968-0004 figure 1 ---	1
P,A	BERTIN J ET AL: "THE PYRIN DOMAIN: A NOVEL MOTIF FOUND IN APOPTOSIS AND INFLAMMATION PROTEINS" CELL DEATH AND DIFFERENTIATION, EDWARD ARNOLD, OXFORD, GB, vol. 12, no. 7, December 2000 (2000-12), pages 1273-1274, XP008006072 ISSN: 1350-9047 the whole document ---	1
P,A	MARTINON F ET AL: "The pyrin domain: a possible member of the death domain-fold family implicated in apoptosis and inflammation." CURRENT BIOLOGY: CB. ENGLAND 20 FEB 2001, vol. 11, no. 4, 20 February 2001 (2001-02-20), pages R118-R120, XP002212417 ISSN: 0960-9822 the whole document ---	1
P,A	WO 01 61005 A (BERTIN JOHN ;MILLENNIUM PHARM INC (US)) 23 August 2001 (2001-08-23) the whole document ---	1
X	DATABASE EMBL 'Online! Acc. No.: AC022066, 26 January 2000 (2000-01-26) BIRREN B ET AL: "Homo sapiens clone RP11-394L10" XP002212594 Sequence with 94.3% identity with SEQ ID No:15 over 1792 nucleotides abstract ---	1-4,15, 16
A	DATABASE EMBL 'Online! Acc. No. P29315, 1 December 1992 (1992-12-01) KAWANOMOTO M ET AL: "Ribonuclease inhibitor" XP002212418 Sequence with 35.2% identity with SEQ ID No:16 over 352 amino acids abstract ---	1-4, 15-18, 25,26

-/-

INTERNATIONAL SEARCH REPORT

national Application No
PCT/US 01/30160

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT		
Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
T	<p>DATABASE EMBL 'Online! Acc. No.: AF442488.1, 26 November 2001 (2001-11-26) MARTINON F ET AL: "NALP4 a novel member of the PYD, NACHT, and LRR family" XP002212419 Sequence with 99.9% identity with SEQ ID No:15 over 2985 nucleotides abstract</p> <p>-----</p>	<p>1-4, 15-18, 25,26</p>

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US 01/30160

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☒ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
Although claim 49 is directed to a method of treatment of the human/animal body, the search has been carried out and based on the alleged effects of the compound/composition.
2. ☐ Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:
1-4, 15-18, 25-33, 37-39, and 49 all partially

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

1. Claims: 1-4, 15-18, 25-33, 37-39, and 49 all partially

Isolated nucleic acids, polypeptides, vectors, cells, antibodies and methods relating to the PAN2 molecule (SEQ ID Nos:15 and 16)

2. Claims: 1-4, 15-18, 25-33, 37-39, and 49 all partially

Isolated nucleic acids, polypeptides, vectors, cells, antibodies and methods relating to the PAN3 molecule (SEQ ID Nos:17 and 18)

3. Claims: 1-4, 15-18, 25-33, 37-39, and 49 all partially

Isolated nucleic acids, polypeptides, vectors, cells, antibodies and methods relating to the PAN4 molecule (SEQ ID Nos:19 and 20)

4. Claims: 1-4, 15-18, 25-33, 37-39, and 49 all partially

Isolated nucleic acids, polypeptides, vectors, cells, antibodies and methods relating to the PAN5 molecule (SEQ ID Nos:21 and 22)

5. Claims: 1-4, 15-18, 25-33, 37-39, and 49 all partially

Isolated nucleic acids, polypeptides, vectors, cells, antibodies and methods relating to the PAN6 molecule (SEQ ID Nos:23 and 24)

6. Claims: 1-4, 15-18, 25-33, 37-39, and 49 all partially

Isolated nucleic acids, polypeptides, vectors, cells, antibodies and methods relating to the pyrin2 molecule (SEQ ID Nos:25 and 26)

7. Claims: 1-4, 15-18, 25-33, 37-39, and 49 all partially

Isolated nucleic acids, polypeptides, vectors, cells, antibodies and methods relating to the ASC2 molecule (SEQ ID Nos:27 and 28)

8. Claims: 5-8, 19, 20, 34, 40, 43-46 and 48 all partially

Isolated nucleic acids, polypeptides, vectors, cells and methods relating to the PAAD domain of PAN2 (SEQ ID No:2)

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

9. Claims: 5-8, 19, 20, 34, 40, 43-46 and 48 all partially

Isolated nucleic acids, polypeptides, vectors, cells and methods relating to the PAAD domain of PAN3 (SEQ ID No:3)

10. Claims: 5-8, 19, 20, 34, 40, 43-46 and 48 all partially

Isolated nucleic acids, polypeptides, vectors, cells and methods relating to the PAAD domain of PAN4 (SEQ ID No:4)

11. Claims: 5-8, 19, 20, 34, 40, 43-46 and 48 all partially

Isolated nucleic acids, polypeptides, vectors, cells and methods relating to the PAAD domain of PAN5 (SEQ ID No:5)

12. Claims: 5-8, 19, 20, 34, 40, 43-46 and 48 all partially

Isolated nucleic acids, polypeptides, vectors, cells and methods relating to the PAAD domain of PAN6 (SEQ ID No:6)

13. Claims: 5-8, 19, 20, 34, 40, 43-46 and 48 all partially

Isolated nucleic acids, polypeptides, vectors, cells and methods relating to the PAAD domain of pyrin2 (SEQ ID No:8)

14. Claims: 5-8, 19, 20, 34, 40, 43-46 and 48 all partially

Isolated nucleic acids, polypeptides, vectors, cells and methods relating to the PAAD domain of ASC2 (SEQ ID No:10)

15. Claims: 9-11, 21, 22, 35, 41 and 47 all partially

Isolated nucleic acids, polypeptides, vectors, cells and methods relating to the NB-ARC domain of PAN2 (SEQ ID No:37)

16. Claims: 9-11, 21, 22 all partially

Isolated nucleic acids, polypeptides, vectors, cells and methods relating to the NB-ARC domain of PAN3 (SEQ ID No:60)

17. Claims: 9-11, 21, 22 all partially

Isolated nucleic acids, polypeptides, vectors, cells and methods relating to the NB-ARC domain of PAN5 (SEQ ID No:62)

18. Claims: 9-11, 21, 22 all partially

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Isolated nucleic acids, polypeptides, vectors, cells and
methods relating to the NB-ARC domain of PAN6 (SEQ ID No:63)

19. Claims: claims 12-14, 23, 24, 36, and 42 all partially

Isolated nucleic acids, polypeptides, vectors, cells and
methods relating to the LRR domain of PAN2 (SEQ ID No:39)

20. Claims: claims 12-14, 23, 24 all partially

Isolated nucleic acids, polypeptides, vectors, cells and
methods relating to the LRR domain of PAN3 (SEQ ID No:61)

21. Claims: claims 12-14, 23, 24 all partially

Isolated nucleic acids, polypeptides, vectors, cells and
methods relating to the LRR domain of PAN6 (SEQ ID No:64)

INTERNATIONAL SEARCH REPORT

Information on patent family members

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